

DOCKET NO.: 221519US0PCT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

IN RE APPLICATION OF: Seiko HIRANO, et al.

SERIAL NO.: NEW U.S. PCT APPLICATION

FILED: HEREWITH

INTERNATIONAL APPLICATION NO.: PCT/JP00/06913

INTERNATIONAL FILING DATE: October 4, 2000

FOR: GENES FOR HEAT RESISTANT ENZYMES OF AMINO ACID BIOSYNTHETIC PATHWAY DERIVED FROM THERMOPHILIC CORYNEFORM BACTERIA

**REQUEST FOR PRIORITY UNDER 35 U.S.C. 119
AND THE INTERNATIONAL CONVENTION**

Assistant Commissioner for Patents
Washington, D.C. 20231

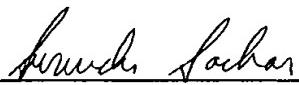
Sir:

In the matter of the above-identified application for patent, notice is hereby given that the applicant claims as priority:

<u>COUNTRY</u>	<u>APPLICATION NO</u>	<u>DAY/MONTH/YEAR</u>
Japan	11/282716	04 October 1999
Japan	11/311147	01 November 1999
Japan	2000/120687	21 April 2000

Certified copies of the corresponding Convention application(s) were submitted to the International Bureau in PCT Application No. PCT/JP00/06913. Receipt of the certified copy(s) by the International Bureau in a timely manner under PCT Rule 17.1(a) has been acknowledged as evidenced by the attached PCT/IB/304.

Respectfully submitted,
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10-089057
PCT/JP00/06913

24.11.00

日本国特許庁
PATENT OFFICE
JAPANESE GOVERNMENT

JPO/6913

別紙添付の書類に記載されている事項は下記の出願書類に記載されて
いる事項と同一であることを証明する。

This is to certify that the annexed is a true copy of the following application as filed
with this Office.

出願年月日
Date of Application:

2000年 4月21日

RECD 08 DEC 2000

PCT

出願番号
Application Number:

特願2000-120687

出願人
Applicant(s):

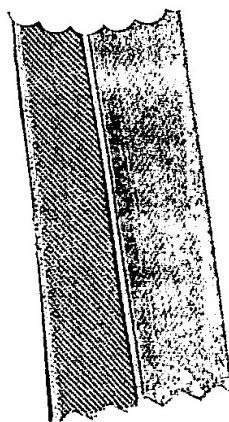
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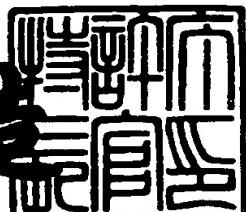
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2000年11月10日

特許庁長官
Commissioner,
Patent Office

及川耕造



出証番号 出証特2000-3093623

【書類名】 特許願
【整理番号】 P-7300
【提出日】 平成12年 4月21日
【あて先】 特許庁長官殿
【国際特許分類】 C12N 15/00
【発明の名称】 高温耐性コリネ型細菌の耐熱性アミノ酸合成系酵素遺伝子
【請求項の数】 14
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特2000-120687

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【連絡先】 03-3669-6571

【先の出願に基づく優先権主張】
【出願番号】 平成11年特許願第311147号
【出願日】 平成11年11月 1日

【手数料の表示】
【予納台帳番号】 012092
【納付金額】 21,000円

【提出物件の目録】
【物件名】 明細書 1
【物件名】 要約書 1

出証特2000-30

特2000-120687

【包括委任状番号】 9117157

【ブルーフの要否】 要

【書類名】明細書

【発明の名称】高温耐性コリネ型細菌の耐熱性アミノ酸生合成系酵素遺伝子

【特許請求の範囲】

【請求項1】配列番号2に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、イソシトレートリアーゼ活性を有するタンパク質をコードするDNA。

【請求項2】配列番号4に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、アシルCo-Aカルボキシラーゼ活性に関与するタンパク質をコードするDNA。

【請求項3】配列番号6に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、DtsR活性を有するタンパク質をコードするDNA。

【請求項4】配列番号8に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、DtsR活性を有するタンパク質をコードするDNA。

【請求項5】配列番号10に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ホスホフルクトキナーゼ活性を有するタンパク質をコードするDNA。

【請求項6】配列番号12又は14に記載のアミノ酸配列、又は、前記アミノ酸配列のいずれかにおいて、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列を含み、かつ、インペルターゼ活性を有するタンパク質をコードするDNA。

【請求項7】配列番号17~20に記載のアミノ酸配列のいずれかを有するタンパク質、又は、前記アミノ酸配列のいずれかにおいて、1若しくは数個の

アミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、グルタミン酸の取り込みに関与する機能を有するタンパク質、をコードするDNA。

【請求項8】 配列番号22に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ピルビン酸デヒドロゲナーゼ活性を有するタンパク質をコードするDNA。

【請求項9】 配列番号24に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ピルビン酸カルボキシラーゼ活性を有するタンパク質をコードするDNA。

【請求項10】 配列番号26に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ホスホエノールピルビン酸カルボキシラーゼ活性を有するタンパク質をコードするDNA。

【請求項11】 配列番号28に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、アコニターゼ活性を有するタンパク質をコードするDNA。

【請求項12】 配列番号30に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、イソクエン酸デヒドロゲナーゼ活性を有するタンパク質をコードするDNA。

【請求項13】 配列番号32に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ジヒドロリボアミドデヒドロゲナーゼ活性を有するタンパク質をコードするDNA。

【請求項14】 配列番号34に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入

、付加、又は逆位を含むアミノ酸配列からなり、かつ、2-オキソグルタル酸デヒドロゲナーゼ活性を有するタンパク質をコードするDNA。

【発明の詳細な説明】

【0001】

【発明の属する技術分野】

本発明は、高温耐性コリネ型細菌であるコリネバクテリウム・サーモアミノゲネスの耐熱性酵素遺伝子、特にL-グルタミン酸等のL-アミノ酸生合成系酵素及び取り込み系遺伝子に関する。

【0002】

【従来の技術】

現在、L-グルタミン酸等のL-アミノ酸の製造は、コリネ型細菌による発酵生産が主流となっている。アミノ酸の発酵生産は、生産能に優れた菌株の育種や発酵技術の開発によって、コストダウンが図られている。従来、コストダウン実現の方向性は、高収率化が主なものであるが、発酵におけるコストとしては、原料以外にも培養中に発生する発酵熱の冷却エネルギーを無視することはできない。すなわち、発酵に用いられている通常の微生物は、発酵中に自らが発生する発酵熱により培地の温度が上昇し、発酵に必要な酵素が失活したり生産菌が死滅したりするために、発酵中に培地を冷却することが必要となっている。したがって、冷却費用を低減するために、高温での発酵に関する検討が古くから行われている。また、高温で発酵を行うことが可能となれば、反応速度を向上させができる可能性もある。しかし、これまでのところ、L-アミノ酸発酵において、有効な高温培養は実現していない。

【0003】

コリネバクテリウム・サーモアミノゲネス (*Corynebacterium thermoaminogenes*) は、L-アミノ酸の発酵に汎用されているコリネバクテリウム・グルタミカム (*Corynebacterium glutamicum*) (ブレビバクテリウム・ラクトファーメンタム (*Brevibacterium lact fermentum*)) 等と同様にコリネ型細菌に分類される細菌であるが、生育至適温度はコリネバクテリウム・グルタミカムの30~35℃に対して37~43℃と高く、L-グルタミン酸生成の至適温度も42~45℃とかなり高

温側にシフトしている（特開昭63-240779号）。

【0004】

ところで、コリネバクテリウム属またはプレビバクテリウム属細菌において、エシェリヒア・コリ又はコリネバクテリウム・グルタミクム由来のL-アミノ酸合成系酵素をコードする遺伝子を導入することにより、同L-アミノ酸の生産能を増強する技術が開発されている。例えば、このような酵素として、例えば、L-グルタミン酸合成系酵素であるクエン酸シンターゼ（特公平7-121228号）、グルタミン酸デヒドロゲナーゼ（特開昭61-268185号）、イソクエン酸デヒドロゲナーゼ、アコニット酸ヒドラターゼ遺伝子（特開昭63-214189号）等がある。

【0005】

しかし、高温耐性のコリネ型細菌由来のL-アミノ酸合成酵素及びそれらをコードする遺伝子は報告されていない。

【0006】

【発明が解決しようとする課題】

本発明は、コリネバクテリウム・サーモアミノゲネス由来の酵素、好ましくはコリネバクテリウム・グルタミカムよりも高い温度で機能する酵素をコードする遺伝子を提供することを課題とする。

【0007】

【課題を解決するための手段】

本発明者は、上記課題を解決するために銳意検討を行った結果、コリネバクテリウム・サーモアミノゲネスのアミノ酸合成系酵素をコードする遺伝子、又はアミノ酸の細胞内への取り込みに関与するタンパク質をコードする遺伝子を単離することに成功し、本発明を完成するに至った。

すなわち本発明は、以下のとおりである。

【0008】

(1) 配列番号2に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、イソシトレートリアーゼ活性を有するタンパク質をコードするDNA。

(2) 配列番号4に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、アシルC_o-Aカルボキシラーゼ活性に関するタンパク質をコードするDNA。

(3) 配列番号6に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、DtsR活性を有するタンパク質をコードするDNA。

【0009】

(4) 配列番号8に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、DtsR活性を有するタンパク質をコードするDNA。

(5) 配列番号10に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ホスホフルクトキナーゼ活性を有するタンパク質をコードするDNA。

(6) 配列番号12又は14に記載のアミノ酸配列、又は、前記アミノ酸配列のいずれかにおいて、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列を含み、かつ、インペルターゼ活性を有するタンパク質をコードするDNA。

【0010】

(7) 配列番号17~20に記載のアミノ酸配列のいずれかを有するタンパク質、又は、前記アミノ酸配列のいずれかにおいて、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、グルタミン酸の取り込みに関する機能を有するタンパク質、をコードするDNA。

(8) 配列番号22に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ピルビン酸デヒドロゲナーゼ活性を有す

るタンパク質をコードするDNA。

(9) 配列番号24に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ピルビン酸カルボキシラーゼ活性を有するタンパク質をコードするDNA。

【0011】

(10) 配列番号26に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ホスホエノールピルビン酸カルボキシラーゼ活性を有するタンパク質をコードするDNA。

(11) 配列番号28に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、アコニターゼ活性を有するタンパク質をコードするDNA。

(12) 配列番号30に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、イソクエン酸デヒドロゲナーゼ活性を有するタンパク質をコードするDNA。

【0012】

(13) 配列番号32に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ジヒドロリポアミドデヒドロゲナーゼ活性を有するタンパク質をコードするDNA。

(14) 配列番号34に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、2-オキソグルタル酸デヒドロゲナーゼ活性を有するタンパク質をコードするDNA。

【0013】

以下、上記の各DNAのいずれか、又はこれらを総称して、本発明のDNAと

いうことがある。

【0014】

【発明の実施の形態】

以下、本発明を詳細に説明する。

本発明のDNAの塩基配列及び遺伝子名、並びに本発明のDNAがコードするタンパク質を以下に示す。

【0015】

【表1】

表1

塩基配列	遺伝子名	コードされるタンパク質
配列番号1	aceA	イソシトレートリアーゼ
配列番号3	accBC	アシルCo-AカルボキシラーゼBCサブユニット
配列番号5	dtsR1	D T S R 1 蛋白質
配列番号7	dtsR2	D T S R 2 蛋白質
配列番号9	pfk	ホスホフルクトキナーゼ
配列番号11, 13, 15	scrB	インペルターゼ
配列番号16	gluABCD	グルタミン酸取り込み系
配列番号21	pdhA	ビルビン酸デヒドロゲナーゼ
配列番号23	pc	ビルビン酸カルボキシラーゼ
配列番号25	ppc	ホスホエノ-β-ビルビン酸カルボキシラーゼ
配列番号27	acn	アコニターゼ
配列番号29	icd	イソクエン酸デヒドロゲナーゼ
配列番号31	lpd	ジヒドロリボアミドデヒドロゲナーゼ
配列番号33	odhA	2-オキソグルタル酸デヒドロゲナーゼ

【0-016】

尚、配列番号3、23、25、31及び33におけるオープン・リーディング・フレーム(ORF)、及び配列番号16の4番目のORFはいずれもGTGから始まっている。配列表にはこのGTGによりコードされるアミノ酸はバリンとして記載されているが、メチオニンである可能性がある。

【0017】

また、配列番号16は4つのORFを含み、5'側から順にgluA、gluB、gluC及びgluDに対応する。

上記の各DNAは、コリネバクテリウム・サーモアミノゲネスAJ12310株 (FERM BP-1542) の染色体DNAから単離されたものである。但し、AJ12310株は、インペルターゼ活性及びシュークロース資化性を持たず、同株から単離したscrB遺伝子断片には、オープンリーディングフレームが存在しなかったため、配列番号11及び13に示すDNAは、インペルターゼ活性及びシュークロース資化性を有するコリネバクテリウム・サーモアミノゲネスAJ12340株 (FERM BP-1539) 及びAJ12309株 (FERM BP-1541) からそれぞれ単離されたものである。

【0018】

尚、配列番号11、13及び15に示す塩基配列は、scrBの部分配列であって、配列番号11及び13は配列番号12及び14に示すインペルターゼの部分アミノ酸配列をコードしている。

【0019】

目的とする遺伝子の部分断片を含むDNAは、すでに報告されているプレビバクテリウム・ラクトファーメンタム等の種々の微生物の目的とする遺伝子の塩基配列の比較を行い、塩基配列がよく保存されている領域を選択し、その領域の塩基配列に基づいて設計したプライマーを用い、コリネバクテリウム・サーモアミノゲネスの染色体DNAを鑄型とするPCRを行うことによって、取得することができる。得られたDNA断片又はその配列に基づいて作製したプローブを用いたハイブリダイゼーションにより、コリネバクテリウム・サーモアミノゲネスの染色体DNAライブラリーをスクリーニングすることによって、目的とする遺伝子全長を含むDNA断片を得ることができる。また、得られた遺伝子の部分断片を用いてゲノムウォーキングを行うことによっても、目的とする遺伝子全長を含むDNA断片を得ることができる。ゲノムウォーキングと、市販のキット、例えばTaKaRa LA PCR in vitro Cloning Kit (宝酒造(株) 製) を用いて行うことができる。

【0020】

また、本発明により、各遺伝子の塩基配列が明らかとなつたので、それらの塩基配列に基づいて作製したプライマーを用いたPCRによって、コリネバクテリウム・サーモアミノゲネスの染色体DNA又は染色体DNAライブラリーから取得することもできる。

【0021】

染色体DNAの調製、染色体DNAライブラリーの作製、ハイブリダイゼーション、PCR、プラスミドDNAの調製、DNAの切断及び連結、形質転換等の方法は、Sambrook,J.,Fritsch,E.F.,Maniatis,T.,*Molecular Cloning*, Cold Spring Harbor Laboratory Press,1.21(1989)に記載されている。

【0022】

次に、本発明のDNAを取得する具体的な方法を例示する。

まず、コリネバクテリウム・サーモアミノゲネスの染色体DNAを、適当な制限酵素、例えばSau3AIで消化し、アガロースゲル電気泳動により分画して約4~6 kbのDNAフラグメントを取得する。得られたDNAフラグメントをpHSG399等のクローニングベクターに挿入し、得られた組換えプラスミドでエシェリヒア・コリを形質転換して、染色体DNAのプラスミドライブラリーを作製する。

【0023】

一方、プラスミドライブラリーから目的の遺伝子を含むクローンをPCRにより選択するために用いるプライマーを作製する。このプライマーは、目的とする遺伝子に対応する種々の微生物の既知の遺伝子配列の間でアミノ酸レベルで保存されている領域に基づいて設計する。その際、コリネ型細菌のコドンユーセージを考慮してプライマーを複数組づつ設計する。

【0024】

次に、作製されたプライマーの適正を調べるために、これらのプライマーを用いて、コリネバクテリウム・サーモアミノゲネスの染色体DNAを錆型としてPCRを行う。そして、增幅断片が得られたプライマーをスクリーニング用プライマーとして用い、プラスミドライブラリーから調製した組換えプラスミドを錆型としてPCRを行い、目的とするDNA断片を含むクローンを選択する。この操作は、一次スクリーニングとして形質転換体数十株を含むバッチ毎に行い、二次

スクリーニングとして増幅断片が得られたバッチについてコロニーPCRを行うことにより、迅速に行うことができる。尚、増幅された遺伝子の断片長は、表2～7に記載した。

【0025】

上記のようにして選択された形質転換体から組換えDNAを調製し、挿入断片の塩基配列をダイ・デオキシ・ターミネーション法等により決定し、塩基配列を既知の遺伝子配列と比較することによって、目的の遺伝子を含むことを確認する。

【0026】

得られたDNA断片が、目的とする遺伝子の一部を含んでいる場合には、ゲノムウォーキングにより欠失部分を取得する。

本発明のDNAは、コードされるタンパク質が本来の機能を有する限り、1若しくは複数の位置での1若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むタンパク質をコードするものであってもよい。ここで、「数個」とは、アミノ酸残基のタンパク質の立体構造における位置や種類によっても異なるが、一般的に、それぞれのタンパク質のアミノ酸配列全体に対し、30から40%以上、好ましくは55～65%以上の相同性を有することが好ましい。具体的には、前記「数個」は、2～数百個、好ましくは、2～数十個、より好ましくは2～10個である。

【0027】

上記のような本来のタンパク質と実質的に同一のタンパク質をコードするDNAは、例えば部位特異的変異法によって、特定の部位のアミノ酸残基が置換、欠失、挿入、付加、又は逆位を含むように、それぞれのタンパク質をコードするDNAの塩基配列を改変することによって得られる。また、上記のような改変されたDNAは、従来知られている変異処理によっても取得され得る。変異処理としては、目的の遺伝子をコードするDNAをヒドロキシルアミン等でインピトロ処理する方法、及び目的の遺伝子をコードするDNAを保持する微生物、例えばエシェリヒア属細菌を、紫外線照射またはN-メチル-N'-ニトロ-N-ニトロソグアニジン(NTG)もしくは亜硝酸等の通常変異処理に用いられている変異剤によ

って処理する方法が挙げられる。

【0028】

また、上記のような塩基の置換、欠失、挿入、付加、又は逆位等には、コリネバクテリウム・サーモアミノゲネスの菌株の違い等に基づく場合などの天然に生じる変異（mutant又はvariant）も含まれる。

【0029】

変異を有するDNAを、適当な細胞で発現させ、発現産物のタンパク質の活性又は機能を調べることにより、本来のタンパク質と実質的に同一のタンパク質をコードするDNAが得られる。また、そのようなDNAは、変異を有するタンパク質をコードするDNAまたはこれを保持する細胞から、例えば表1に示す各配列番号の塩基配列を有するDNA又はその塩基配列から調製されるプローブとストリンジエントな条件下でハイブリダイズし、かつ、当該タンパク質が本来有する活性を示すタンパク質をコードするDNAを単離することによっても得ることができる。

【0030】

上記プローブは、表1に示す各配列番号の塩基配列を有するDNA、又はそれらの塩基配列を有するDNAから、適当なプライマーを用いてPCRにより調製することができる。

【0031】

上記でいう「ストリンジエントな条件」とは、いわゆる特異的なハイブリッドが形成され、非特異的なハイブリッドが形成されない条件をいう。この条件を明確に数値化することは困難であるが、一例を示せば、相同性が高いDNA同士、例えば50%以上の相同性を有するDNA同士がハイブリダイズし、それより相同性が低いDNA同士がハイブリダイズしない条件、あるいは通常のサザンハイブリダイゼーションの洗いの条件である60℃、1×SSC、0.1%SDS、好ましくは、0.1×SSC、0.1%SDSに相当する塩濃度でハイブリダイズする条件が挙げられる。

【0032】

このような条件でハイブリダイズする遺伝子の中には途中にストップコドンが

発生したものや、活性中心の変異により活性を失ったものも含まれるが、それらについては、市販の活性発現ベクターにつなぎ、活性又は機能を調べることによって容易に取り除くことができる。

【0033】

本発明のDNAを、適当な宿主-ベクター系を用いて発現させることにより、それぞれのDNAに対応したタンパク質を製造することができる。

遺伝子の発現に用いる宿主としては、ブレビバクテリウム・ラクトファーメンタム（コリネバクテリウム・グルタミカム）、コリネバクテリウム・サーモアミノゲネス等のコリネ型細菌、エシェリヒア・コリ、バチルス・ズブチリスをはじめとする種々の原核細胞、サッカロマイセス・セレビシエ (*Saccharomyces cerevisiae*) をはじめとする種々の真核細胞、動物細胞、植物細胞が挙げられるが、これらの中では原核細胞、特にコリネ型細菌及びエシェリヒア・コリが好ましい。

【0034】

本発明のDNAは、エシェリヒア・コリ及び／又はコリネ型細菌等の細胞内において自律複製可能なベクターDNAに接続して組換えDNAを調製し、これをエシェリヒア・コリ細胞に導入しておくと、後の操作がしやすくなる。エシェリヒア・コリ細胞内において自律複製可能なベクターとしては、プラスミドベクターが好ましく、宿主の細胞内で自立複製可能ものが好ましく、例えば pUC19、pUC18、pBR322、pHSG299、pHSG399、pHSG398、RSF1010等が挙げられる。

【0035】

コリネ型細菌の細胞内において自律複製可能なベクターとしては、pAM330（特開昭58-67699号公報参照）、pHM1519（特開昭58-77895号公報参照）等が挙げられる。また、これらのベクターからコリネ型細菌中でプラスミドを自律複製可能にする能力を持つDNA断片を取り出し、前記エシェリヒア・コリ用のベクターに挿入すると、エシェリヒア・コリ及びコリネ型細菌の両方で自律複製可能ないわゆるシャトルベクターとして使用することができる。

【0036】

このようなシャトルベクターとしては、以下のものが挙げられる。尚、それぞ

れのベクターを保持する微生物及び国際寄託機関の受託番号をかっこ内に示した

pAJ655 エシエリヒア・コリAJ11882(FERM BP-136)

コリネバクテリウム・グルタミクムSR8201(ATCC39135)

pAJ1844 エシエリヒア・コリAJ11883(FERM BP-137)

コリネバクテリウム・グルタミクムSR8202(ATCC39136)

pAJ611エシエリヒア・コリAJ11884(FERM BP-138)

pAJ3148 コリネバクテリウム・グルタミクムSR8203(ATCC39137)

pAJ440バチルス・ズブチリスAJ11901(FERM BP-140)

pHC4 エシエリヒア・コリAJ12617(FERM BP-3532)

【0037】

本発明のDNAとコリネ型細菌で機能するベクターを連結して組み換えDNAを調製するには、本発明のDNAの末端に合うような制限酵素でベクターを切断する。連結は、T4 DNAリガーゼ等のリガーゼを用いて行うのが普通である。

【0038】

上記のように調製した組み換えDNAをコリネ型細菌等の宿主に導入するには、これまでに報告されている形質転換法に従って行えばよい。例えば、エシエリヒア・コリ K-12について報告されているような、受容菌細胞を塩化カルシウムで処理してDNAの透過性を増す方法 (Mandel, M. and Higa, A., J. Mol. Biol., 53, 159 (1970)) があり、バチルス・ズブチリスについて報告されているような、増殖段階の細胞からコンピテントセルを調製してDNAを導入する方法 (Duncan, C.H., Wilson, G.A. and Young, F.E., Gene, 1, 153 (1977)) がある。あるいは、バチルス・ズブチリス、放線菌類及び酵母について知られているような、DNA受容菌の細胞を、組換えDNAを容易に取り込むプロトプラストまたはスフェロプラストの状態にして組換えDNAをDNA受容菌に導入する方法 (Chang, S. and Cho, S.N., Molec. Genet., 168, 111 (1979); Bibb, M.J., Ward, J.M. and Hopwood, J.A., Nature, 274, 398 (1978); Hinnen, A., Hicks, J.B. and Fink, G.R., Proc. Natl. Acad. Sci. USA, 75, 1929 (1978)) も応用できる。コリネ型細菌においては、電気パルス法 (特開平2-207791号公報参照) が有効

である。

【0039】

本発明のDNAに含まれる遺伝子の発現を効率的に実施するために、これらの遺伝子のコード領域の上流に、宿主細胞内で働くlac、trp、 P_L 等のプロモーターを連結してもよい。ベクターとして、プロモーターを含むベクターを用いること、各遺伝子と、ベクター及びプロモーターとの連結を一度に行なうことができる。

【0040】

上記のようにして製造されるタンパク質は、必要に応じて、菌体抽出液又は培地からイオン交換クロマトグラフィー、ゲル濾過クロマトグラフィー、吸着クロマトグラフィー、塩析、溶媒沈殿等、通常の酵素の精製法を用いて精製することができる。

【0041】

本発明のDNAのうち、pfk、pdhA、pc、ppc、acn及びicdは、コリネ型細菌等のL-アミノ酸生産菌に導入することによって、L-アミノ酸生産能を高めることができる。また、本発明のDNAが導入されたコリネ型細菌は、通常よりも高い温度でのL-アミノ酸の生産が可能となることが期待される。L-アミノ酸としては、L-グルタミン酸、L-アスパラギン酸、L-リジン、L-アルギニン、L-プロリン及びL-グルタミン等が挙げられる。

【0042】

また、dtsR1及びdtsR2は、コリネ型細菌に界面活性剤に対する耐性を付与する蛋白質(DTSR蛋白)をコードする遺伝子であり、これらの遺伝子が破壊されたコリネ型L-グルタミン酸生産菌は、野生株がほとんどL-グルタミン酸を生成しない量のビオチンが存在する条件においても著量のL-グルタミン酸を生成する。また、L-リジン生産能を有するコリネ型L-グルタミン酸生産菌は、dtsR1及びdtsR2遺伝子を増幅すると、著量のL-リジンを生産する能力が付与される(WO95/23224号国際公開パンフレット、特願平10-234371号公報)。

【0043】

scrB遺伝子は、シュークロースを含む培地でコリネ型細菌を用いてL-アミノ

酸を製造する場合に、同コリネ型細菌の育種に用いることができる。

コリネ型細菌等のL-グルタミン酸生産菌において、のacA、accBC、lpd又はodhAを欠失させることにより、L-グルタミン酸生産性を高めることができる。また、gluABCDはL-グルタミン酸の取り込み系の遺伝子クラスターであり、コリネ型L-グルタミン酸生産菌において、gluA、gluB、gluCもしくはgluD、又はこれらの1種、2種、3種もしくは4種を欠失させることにより、培地に蓄積されるL-グルタミン酸量を増大させることができる。本発明のaceA、accBC、lpd、odhA及びgluABCDは、染色体上のこれらの遺伝子を破壊するのに用いることができる。

【0044】

【実施例】

以下、本発明を実施例によりさらに具体的に説明する。

【0045】

<1>コリネバクテリウム・サーモアミノゲネスのプラスミドライブラーの作製

コリネバクテリウム・サーモアミノゲネス AJ12310株を、CM2B液体培地（イーストエキストラクト（Difco社製）1g/dl、ポリペプトン（日本製薬製）1g/dl、NaCl 0.5g/dl、ビオチン 10 μg/dl、pH 7.0（KOHで調整））で37℃にて15時間培養し、10mlの培養液から、染色体DNAを染色体DNA抽出キット（Bacterial Genome DNA Purification Kit (Advanced Genetic Technologies社製)）を用いて取得した。取得したDNAを、制限酵素Sau3AIを用いて部分消化し、0.8%アガロースゲル電気泳動を行い、DNAを分画した後に、約4～6kbのDNAフラグメントをゲルから切り出し、DNAゲル抽出キット（GIBCO BRL社、ConcertTMRapid Gel Extraction System）を用いて、目的サイズのDNA断片を取得した。

【0046】

プラスミドpHSG399（宝酒造（株）製）をBamHIで完全消化し、末端をアルカリフォスファターゼ（CIAP；宝酒造（株）製）を用いて脱リン酸化した。このベクター断片と、上記の染色体DNA断片を宝酒造社製DNAライゲーションキットを用いて連結し、得られた組換えベクターを用いてエシェリヒア・コリ JM109を形質転

換した。形質転換体の選択は、 $30\mu\text{g}/\text{ml}$ のクロラムフェニコール、 $0.04\text{mg}/\text{ml}$ の IPTG (イソプロピル- β -D-チオガラクトピラノシド)、 $0.04\text{mg}/\text{ml}$ のX-Gal (5-ブロモ-4-クロロ-3-インドリル- β -D-ガラクトシド) を含むLB寒天培地 (寒天 $1.5\text{g}/\text{dl}$ を含む) 上にて行い、白色コロニーを約4000コロニー取得した。

【0047】-----

<2>各遺伝子断片增幅用プライマーの設定

上記で得られたプラスミドライブラーから目的の遺伝子を含むクローンをPCRにより選択するために用いるプライマーを設計した。目的とする遺伝子は前記のとおりである。

【0048】

プライマーは、コリネ型細菌の既知の遺伝子配列をベースとして、他の微生物の相当する遺伝子との間でアミノ酸レベルで保存されている領域に基づいて設計した。その際、コリネ型細菌のコドンユーセージを考慮してプライマーを複数組づつ設計した。

【0049】

作製されたプライマーの適正を調べるために、これらのプライマーを用いて、コリネバクテリウム・サーモアミノゲネスAJ12310株の染色体DNAを鑄型としてPCRを行い、遺伝子断片を増幅した。その結果、いずれの遺伝子も、表2～表7の上段に示すプライマーを用い、各表中に「部分断片取得のPCR」として示した条件及びポリメラーゼでPCRを行った場合に、増幅断片が認められた。各プライマーの末尾のカッコ内の数字は、配列表中の配列番号を示す。これらのプライマーを、後述のスクリーニング用プライマーとして用いた。

【0050】

【表2】

2
版

[0051]

【表3】

表3

遺伝子名	dtsR2	pfk	scrB
5'→3'リバース 3'→5'リバース	ACGGCCAGCCTGACCGAC (41) AGCAGGCCATGACGGCA (42)	CGTCATCCGAGGAATCCTCC (43) CGTGGCCCCATGACCTCC (44)	GGNCGHYTBAAGAYGCC (45) GGRCAYTCCCACATRTANCC (46)
部分断片取得のPCR 条件及びPCRの条件	94°C 5min 98°C 5sec 66°C 2sec 30 cycle Z-Taq	94°C 5min 98°C 5sec 66°C 2sec 30 cycle Z-Taq	94°C 5min 98°C 5sec 50°C 10sec 72°C 20sec 40 cycle Z-Taq
DN-PCRの条件	94°C 7min 91°C 30sec 55°C 1sec 72°C 2.5min 30 cycle Ex-Taq	94°C 7min 91°C 30sec 55°C 1sec 72°C 2.5min 30 cycle Ex-Taq	94°C 7min 91°C 30sec 55°C 1sec 72°C 2.5min 30 cycle Ex-Taq
增幅断片	806bp	472bp	500bp

【0052】

【表4】

表4

遺伝子名	gluABCD	pdhA
5'→3' 7°ライマー 3'→5' 7°ライマー	CCATCCGGATCCGGCAAGTC (47) AATCCCATCTCGTGGGTAAAC (48)	ACTGTGTCCATGGGTCTTGGCCC (49) CGCTGGAATCCAACATCGA (50)
部分断片 取得の PCR条件	94°C 5min 98°C 5sec 50°C 10sec 72°C 20sec 30 cycle Z-Taq	94°C 5min 98°C 5sec 50°C 10sec 72°C 20sec 30 cycle Z-Taq
增幅断片	500bp	1200bp
スクリーニング*PCR ヨロニ-PCR の条件	94°C 5min 94°C 30sec 50°C 1min 72°C 2min 30 cycle EX-Taq	94°C 5min 94°C 30sec 50°C 1min 72°C 2min 30 cycle EX-Taq

【0053】

【表5】

表5

遺伝子名	pc	ppc
5'→3'アライヤー 3'→5'アライヤー	GGCGAACCTACGACGTTGCAATGCG (51) TGGCCGCCTGGATCTCGTG (52)	GGTCCTGGATTGGTGGAGA (53) CCGCCATCCTGTTGGAATC (54)
部分断片 取得の PCR条件	94°C, 5min 98°C, 5sec 55°C, 80sec 30 cycle Z-Taq	94°C 5min 98°C 5sec 50°C 5sec 72°C 10sec 30 cycle Z-Taq
增幅断片	781bp	1000bp
スクリーニングPCR の条件	94°C, 5min 98°C, 5sec 55°C, 80sec 30 cycle Z-Taq	94°C 5min 98°C 5sec 50°C 5sec 72°C 10sec 30 cycle Z-Taq
JUN-PCR の条件	94°C, 5min 1 cycle 98°C, 5sec 55°C, 80sec 50 cycle Z-Taq	94°C 5min 98°C 5sec 50°C 10sec 72°C 20sec 50 cycle Z-Taq

【0054】

【表6】

表6

遺伝子名	acn	icd	lpd
5'→3' 7'ライ- 3'→5' 7'ライ-	GTIGGIACIGAYTCSCATAC (55) GCIGGAGAIATGTRTCIGT (56)	GACATTTCACTCGCTGGACG (57) CCGTAECTTCAGCCTCTG (58)	ATCATCGAACCGGTTC (59) CGTCACCGATGGCGTAAAT (60)
部分断片 取得の PCR条件	94°C 1min 96°C 20sec 45°C 1min 68°C 2min 30 cycle EX-Taq	94°C 5min 98°C 5sec 55°C 80sec 30 cycle Z-Taq	94°C 5min 98°C 5sec 50°C 10sec 72°C 20sec 30 cycle Z-Taq
増幅断片	1500bp	1500bp	500bp
スクリーニング PCR ヨニ-PCR の条件	同上	同上	94°C 5min 94°C 30sec 57°C 1min 72°C 1min 30 cycle Ex-Taq
スクリーニング PCR 5'→3' 7'ライ- 3'→5' 7'ライ-			TACGAGGAGCAGATCCTCAA (63) TTGACGCCGGTGTCTCCAG (64)
LAクローニング (N°) 3'→5' 7'ライ-	S1:GGTGAAAGCTAAGTAGTTAGC (65) S2:AGCTACTAAACCTGCACC (66)	S1:CCGTACTCTTCAGCCTCTG (67) S2:TCGTCCCTGTTCACATC (68)	S1:ATCATCGAACCGGTTC (69) S2:TACGAGGAGCAGATCCTCAA (70)
LAクローニング (C°) 5'→3' 7'ライ-	S1:GCTAACTACTTAGCTTCACC (71) S2:GAACCCAGGAACATTGAACC (72)	S1:TCCGATGTCATCATGAC (73) S2:ATGTGGAACAAGGACGAC (74)	
制限酵素	PstI(N°) HindIII(C°)	Sall(N°) PstI(C°)	HindIII
LAクローニング の条件	N° 94°C 1min 94°C 30sec 57°C 2min 72°C 2min 30 cycle LA-Taq	94°C 1min 94°C 30sec 57°C 2min 72°C 2.5min 30 cycle LA-Taq	94°C 1min 94°C 30sec 57°C 2min 72°C 1min 30 cycle LA-Taq
	C° 94°C 1min 94°C 30sec 57°C 2min 72°C 2.5min 30 cycle LA-Taq		

【0055】

【表7】

表7

遺伝子名	odhA
5'→3' プライマー 3'→5' プライマー	ACACCGTGGTCGCCTAACG (61) TGCTAACCGTCCCACCTGG (62)
部分断片 取得の PCR条件	94°C 5min 98°C 5sec 66°C 2sec 30 cycle Z-Taq
增幅断片	1306bp
LAクローニング (N°) 5'→3' プライマー	S1:GTACATATTGTCGTTAGAACGCGTAATACGACTCA (75) S2:CGTTAGAACGCGTAATACGACTCACTATAGGGAGA (76)
制限酵素	XbaI
LAクローニング の条件	1回目 94°C 30sec 55°C 2min 72°C 1min 30cycle LA-Taq 2回目 94°C 1min 98°C 20sec 68°C 15min 30 cycle 72°C 10min LA-Taq

<3> PCRによるプラスミドライブラーのスクリーニング

前記のプラスミドライブラーから目的の遺伝子を含むクローンを、PCRにより選択した。プラスミドライブラーから、コロニーを60個ずつピックアップし、2枚づつのLB寒天培地プレートにレプリカした。各プレートのコロニー60個づつをまとめて、4mlのLB液体培地を含む試験管に接種し、15時間培養した後、プロメガ社製プラスミドDNA抽出キットを用いてそれぞれプラスミドの混合物を取得した。このプラスミド混合物を鋳型とし、各目的遺伝子毎に作製したスクリーニング用プライマーを用いて、各表中に「スクリーニングPCRの条件」と

して示した条件でPCRを行い、染色体DNAを鑄型とするPCRと同じ大きさのDNA断片が増幅されるクローンを選択した。

【0056】

増幅されたDNA断片は、パーキンエルマー社製ピッグダイ・ダイターミネーターサイクルシークエンスキットを用いて塩基配列を決定し、既知の遺伝子情報との相同意を比較することにより、目的遺伝子の取得の成否を確認した。

【0057】

尚、1pdについては、<2>で作製したプライマーでは目的のDNA断片が増幅されなかったので、決定された塩基配列に基づいて、スクリーニング用プライマーを別途作製した。

【0058】

<4>コロニーPCRによる目的遺伝子保持クローンの選択

目的の遺伝子断片の増幅が確認されたプラスミド混合物が由来するプレートを用いて、コロニーPCRを行い、遺伝子断片を含むクローンを選択した。コロニーPCRは、表2～7に示す条件で行った。

【0059】

選択された形質転換体からプラスミドDNAを回収し、挿入DNA断片の塩基配列を決定した。挿入DNA断片に目的遺伝子の全長が挿入されておらず、遺伝子の上流域、下流域またはこれらの両方が欠失している場合は、判明した塩基配列を利用してプライマーを作製し、Takara LA PCR in vitro Cloning Kit（宝酒造（株））を用いて、目的遺伝子の全領域の遺伝子断片を取得し、塩基配列を決定した。

【0060】

LA PCRクローニングの概要は以下のとおりである。挿入DNA断片のうち2つの領域の塩基配列を有する2種のプライマーを作製する。コリネバクテリウム・サーモアミノゲネスAJ12310株の染色体DNAを各種制限酵素で切断し、各制限酵素に対応したカセットプライマーと連結する。これを鑄型として、作製されたプライマーのうち欠失部分から遠い位置に対応するプライマー（S1）と、カセットプライマーの外側の位置に対応するカセットプライマー（C1）を用いてP

CRを行う。次に、作製されたプライマーのうち欠失部分に近い位置に対応するプライマー（S2）と、カセットプライマーの内側の位置に対応するカセットプライマー（C2）を用いてPCRを行う。こうして、欠失部分を含むDNA断片が得られる。得られたDNA断片と既に取得されているDNA断片を連結することにより、目的遺伝子全長を含むDNA断片を得ることができる。尚、カセットの5'末端にはリン酸基が付いていないので、DNA断片の3'末端とカセットの5'末端との接続部位にはニックができる。そのため、1回目のPCRではプライマーC1からのDNA合成はこの接続部分でストップし、非特異的な増幅は起こらないため、特異的な増幅を行うことができる。

【0061】

LA PCRクローニングに用いたプライマーと反応条件は、表2～7に示した。表中「(N')」は上流側の欠失部分のクローニングに用いたプライマーを、「(C')」は下流側の欠失部分のクローニングに用いたプライマーを、それぞれ示す。また、PCR反応はLA PCRクローニングキットの説明書に従い、2回行った。表に示したプライマーのうち、上段には1回目の反応に用いたプライマー（S1）を、下段には2回目の反応に用いたプライマー（S2）を示す。

【0062】

上記のようにして得られた各遺伝子を含むDNA断片の塩基配列を、前記と同様にして決定した。それらの塩基配列及び同塩基配列がコードし得るアミノ酸配列を、配列番号1～34に示す。各配列番号に記載された配列は、下記のとおりである。

【0063】

scrBについては、オープン・リーディング・フレームが見つからなかった。コリネバクテリウム・サーモアミノゲネス AJ12310株は、インペルターゼ活性をしておらず、シュークロース資化性を持たないため、シュークロース資化性を有するコリネバクテリウム・サーモアミノゲネス YS-40株及びYS-155株から、同様にしてscrB遺伝子断片を取得した。その結果、いずれの株からもオープン・リーディング・フレームを有するDNA断片が得られた。

【0064】

配列番号1 : aceA 塩基配列
配列番号2 : aceA アミノ酸配列
配列番号3 : accBC塩基配列
配列番号4 : accBCアミノ酸配列
配列番号5 : dtsR1塩基配列
配列番号6 : dtsR1アミノ酸配列
配列番号7 : dtsR2塩基配列
配列番号8 : dtsR2アミノ酸配列
配列番号9 : pfk塩基配列
配列番号10 : pfkアミノ酸配列
配列番号11 : scrB 塩基配列
配列番号12 : scrB アミノ酸配列
配列番号13 : scrB 塩基配列
配列番号14 : scrB アミノ酸配列
配列番号15 : scrB 塩基配列
配列番号16 : gluABCD塩基配列
配列番号17 : gluABCDアミノ酸配列
配列番号18 : gluABCDアミノ酸配列
配列番号19 : gluABCDアミノ酸配列
配列番号20 : gluABCDアミノ酸配列
配列番号21 : pdhA 塩基配列
配列番号22 : pdhA アミノ酸配列
配列番号23 : pc 塩基配列
配列番号24 : pc アミノ酸配列
配列番号25 : ppc塩基配列
配列番号26 : ppcアミノ酸配列
配列番号27 : acn塩基配列
配列番号28 : acnアミノ酸配列
配列番号29 : icd塩基配列

配列番号30： icdアミノ酸配列

配列番号31： lpd塩基配列

配列番号32： lpdアミノ酸配列

配列番号33： odhA 塩基配列

配列番号34： odhA アミノ酸配列

【0065】

【発明の効果】

本発明により、コリネバクテリウム・サーモアミノゲネスのアミノ酸生合成系酵素をコードする遺伝子、又はアミノ酸の細胞内への取り込みに関与するタンパク質をコードする遺伝子が提供される。

本発明の遺伝子は、前記酵素又はタンパク質の製造、又はアミノ酸生産菌の育種に利用することができる。

【0066】

【配列表】

SEQUENCE LISTING

<110> Ajinomoto, Co., Inc.

<120> 高温耐性コリネ型細菌の耐熱性アミノ酸生合成系酵素遺伝子

<130> P-7300

<140>

<141> 2000-04-21

<150> JP 11-311147

<151> 1999-11-01

<160> 76

<170> PatentIn Ver. 2.0

[0067]

<210> 1

<211> 1980

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (577)..(1869)

<400> 1

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tcgctgcgcc ccagggggag ctggcgatgt gaccaggta agtgataacc atcaccttgc 180
caatgggttt gcgaacttta ccgtgacgct acccccgctt ttgtttgatc acaccagctc 240
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ctcaccatga tgtggggat tcgcatcaca cagtgtgcag ggccggcacct ctaccgaatg 540
cgcccttacag cagcaccaag aagaagtgac tcttag atg tca aac gtt gga acg 594

Met Ser Asn Val Gly Thr

1 - - - - 5 -

cca cgt acc gca cag gaa atc cag cag gat tgg gac acc aac cca cgc 642
Pro Arg Thr Ala Gln Glu Ile Gln Gln Asp Trp Asp Thr Asn Pro Arg

10

15

20

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Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala Glu Gln Val Ala Glu Leu			
25	30	35	
cag ggc agc gtc gtc gag gag cac acc ctc gca aag cgc ggc gcc gag	738		
Gln Gly Ser Val Val Glu Glu His Thr Leu Ala Lys Arg Gly Ala Glu			
40	45	50	
atc ctg tgg gat gca gtt tcc gca gag ggc gac gac tac atc aac gca	786		
Ile Leu Trp Asp Ala Val Ser Ala Glu Gly Asp Asp Tyr Ile Asn Ala			
55	60	65	70
ctg ggc gcc ctt acc ggt aac cag gct gtc cag cag gtc cgt gcc ggc	834		
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75	80	85	
ctg aag gct gtc tac ctc tcc ggc tgg cag gtc gca ggt gac gcc aac	882		
Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln Val Ala Gly Asp Ala Asn			
90	95	100	
ctc gcc ggt cac acc tac ccc gac cag tcc ctg tac ccg gcg aac tcc	930		
Leu Ala Gly His Thr Tyr Pro Asp Gln Ser Leu Tyr Pro Ala Asn Ser			
105	110	115	
gtc ccg aac gtt gtc cgt cgc atc aac aac gca ctg ctg cgc gcc gat	978		
Val Pro Asn Val Val Arg Arg Ile Asn Asn Ala Leu Leu Arg Ala Asp			
120	125	130	
gag atc gca cgc gtc gag ggt gac acc tcc gtc gac aac tgg ctc gtc	1026		
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Lys Val Leu Ile Pro Thr Gln Gln His Ile Arg Thr Leu Asn Ser Ala			
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cgc ctg gca gct gac gtg gcc aac acc ccg acc gtc gtc atc gcc cgc			1266
Arg Leu Ala Ala Asp Val Ala Asn Thr Pro Thr Val Val Ile Ala Arg			
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acc gac gca gag gcc acc ctg atc acc tct gat gtt gat gag cgc			1314
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Val Lys Pro Gly Leu Glu Pro Cys Ile Ala Arg Ala Lys Ser Tyr Ala			
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ccc tac gca gac atg atc tgg atg gag acc ggc acc cct gac ctc gag			1458
Pro Tyr Ala Asp Met Ile Trp Met Glu Thr Gly Thr Pro Asp Leu Glu			
— 280 —	— 285 —	290	
ctg gcc aag aag ttc gcc gag ggc gtc cgc agc gag ttc ccg gac cag			1506
Leu Ala Lys Lys Phe Ala Glu Gly Val Arg Ser Glu Phe Pro Asp Gln			
<u>295</u>	300	305	310
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Leu Leu Ser Tyr Asn Cys Ser Pr Ser Phe Asn Trp Ser Ala His Leu			
315	320	325	
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 Phe Val Asp Leu Gln Asn Arg Glu Phe Lys Ala Ala Glu Glu Arg Gly
 375 380 385 390
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【0068】
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 <211> 431
 <212> PRT
 <213> **Corynebacterium thermoaminogenes**

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 35 40 45
 Ala Lys Arg Gly Ala Glu Ile Leu Trp Asp Ala Val Ser Ala Glu Gly
 50 55 60
 Asp Asp Tyr Ile Asn Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val
 65 70 75 80
 Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln
 85 90 95
 Val Ala Gly Asp Ala Asn Leu Ala Gly His Thr Tyr Pro Asp Gln Ser
 100 105 110
 Leu Tyr Pro Ala Asn Ser Val Pro Asn Val Val Arg Arg Ile Asn Asn
 115 120 125
 Ala Leu Leu Arg Ala Asp Glu Ile Ala Arg Val Glu Gly Asp Thr Ser
 130 135 140
 Val Asp Asn Trp Leu Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe
 145 150 155 160
 Gly Gly Ala Leu Asn Val Tyr Glu Leu Gln Lys Gly Met Ile Thr Ala
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 Gly Ala Ala Gly Thr His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys
 180 185 190
 Cys Gly His Leu Gly Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile
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 Arg Thr Leu Asn Ser Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pr
 210 215 220
 Thr Val Val Ile Ala Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr

225	230	235	240
Ser Asp Val Asp Glu Arg Asp Arg Pro Phe Ile Thr Gly Glu Arg Thr			
245	250	255	
Ala Glu Gly Tyr Tyr His Val Lys Pro Gly Leu Glu Pro Cys Ile Ala			
260	265	270	
Arg Ala Lys Ser Tyr Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr			
275	280	285	
Gly Thr Pro Asp Leu Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg			
290	295	300	
Ser Glu Phe Pro Asp Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe			
305	310	315	320
Asn Trp Ser Ala His Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys			
325	330	335	
Glu Leu Gly Ala Met Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly			
340	345	350	
Phe His Ser Leu Asn Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala			
355	360	365	
Arg Glu Gly Met Pro Ala Phe Val Asp Leu Gln Asn Arg Glu Phe Lys			
370	375	380	
Ala Ala Glu Glu Arg Gly Phe Thr Ala Val Lys His Gln Arg Glu Val			
385	390	395	400
Gly Ala Gly Tyr Phe Asp Thr Ile Ala Thr Thr Val Asp Pro Asn Ser			
405	410	415	
Ser Thr Thr Ala Leu Lys Gly Ser Thr Glu Glu Cys Gln Phe His			
420	425	430	

【0069】

<210> 3

<211> 2381

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (577)..(2349)

<400> 3

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 acacctggtt cgtgttgaag tacctgctgg gtttgaaaaa cgtccgcaac tatgacggtt 180
 cctggtccga gtggggcaac atggtgcgca tgcccatgt ccagggtgat gagccggct 240
 cactctagtc accccggggt cacctccctg gtcacccccc taccctcccc ggtacacccc 300
 ggggacgggg tgtgacctgg atctccctg catgtggaca ccggaaact ttgcctggga 360
 aatgaccatc cagtaccgta atgcgggtat gtaacgcgg tcacaggta caccagaatc 420
 cggatcgct aacccctta gcgggattcg ctaaaagatc accgagttag tgtgcaagaa 480
 taatgctgat cgcagggca ctgtcatacg ctgtcatgca gtcaatgaac agtgcggtgc 540
 tctgtcgtga agaaaatcaa aaccaggagg gttta gtg tca gtc gag acc agg 594

Val Ser Val Glu Thr Arg

1 5

aag atc acc aag gta ctt gtc gcc aac cgt ggt gaa atc gca atc cgt 642

Lys Ile Thr Lys Val Leu Val Ala Asn Arg Gly Glu Ile Ala Ile Arg

10 15 20

gtt ttc cgc gca gca cgg gat gaa ggc atc gcc tct gtc gcc gtc tac 690

Val Phe Arg Ala Ala Arg Asp Glu Gly Ile Ala Ser Val Ala Val Tyr

25 30 35

gcg gag ccg gac gca gat gcc cct ttc gtc gag tat gcc gat gag gcc 738

Ala Glu Pr Asp Ala Asp Ala Pr Phe Val Glu Tyr Ala Asp Glu Ala

40 45 50

ttc gca ctc ggt ggc cag act tcc gca gag tcc tac ctc gtc att gac 786

Phe Ala Leu Gly Gly Gln Thr Ser Ala Glu Ser Tyr Leu Val Ile Asp
 55 60 65 70
 aag atc att gac gca gca cgc aag tcc ggt gca gac gct gtc cac ccc 834
 Lys Ile Ile Asp Ala Ala Arg Lys Ser Gly Ala Asp Ala Val His Pro
 75 80 85
 ggc tac ggc ttc ctc gcc gag aac gcc gat ttc gct gaa gct gtc atc 882
 Gly Tyr Gly Phe Leu Ala Glu Asn Ala Asp Phe Ala Glu Ala Val Ile
 90 95 100
 aac gag ggc ctg atc tgg atc gga cca tcc cct gag tcc atc cgt tcc 930
 Asn Glu Gly Leu Ile Trp Ile Gly Pro Ser Pro Glu Ser Ile Arg Ser
 105 110 115
 ctc ggt gac aag gtc acc gca cgc cac atc gcc aac aac gcc aac gca 978
 Leu Gly Asp Lys Val Thr Ala Arg His Ile Ala Asn Asn Ala Asn Ala
 120 125 130
 ccg atg gca ccg ggc acc aag gag cct gtc aag gac gcc gct gag gtt 1026
 Pro Met Ala Pro Gly Thr Lys Glu Pro Val Lys Asp Ala Ala Glu Val
 135 140 145 150
 gtc gcc ttc gcc gag gag ttc ggt ctc ccc atc gcc atc aag gct gcc 1074
 Val Ala Phe Ala Glu Glu Phe Gly Leu Pro Ile Ala Ile Lys Ala Ala
 155 160 165
 ttc ggt ggc ggc gga cgt ggc atg aag gtc gcc tac gag atg gac gag 1122
 Phe Gly Gly Gly Arg Gly Met Lys Val Ala Tyr Glu Met Asp Glu
 170 175 180
 gtc gcc gac ctc ttc gaa tcc gcc acc cgt gag gcc acc gcc gcc ttc 1170
 Val Ala Asp Leu Phe Glu Ser Ala Thr Arg Glu Ala Thr Ala Ala Phe
 185 190 195
 ggt cgt ggt gag tgc ttc gtg gag cgc tac ctg gac aag gcc cgc cac 1218
 Gly Arg Gly Glu Cys Phe Val Glu Arg Tyr Leu Asp Lys Ala Arg His
 200 205 210

gtc gag gca cag gtc atc gcc gac aag cac ggc aac gtt gtg gtc gcc	1266
Val Glu Ala Gln Val Ile Ala Asp Lys His Gly Asn Val Val Val Ala	
215 220 225 230	
ggt acc cgt gac tgc tcc ctg cag cgt cgt ttc cag aag ctc gtc gag	1314
Gly Thr Arg Asp Cys Ser Leu Gln Arg Arg Phe Gln Lys Leu Val Glu	
235 240 245	
gag gca ccg gca ccg ttc ctc acc gat gag cag cgt gac cgc atc cac	1362
Glu Ala Pro Ala Pro Phe Leu Thr Asp Glu Gln Arg Asp Arg Ile His	
250 255 260	
tcc tcc gcc aag gct atc tgc cgc gag gcc ggt tac tac ggt gcc ggc	1410
Ser Ser Ala Lys Ala Ile Cys Arg Glu Ala Gly Tyr Tyr Gly Ala Gly	
265 270 275	
acc gtg gag tac ctg gtc ggt tcc gac gga ctg atc tcc ttc ctg gag	1458
Thr Val Glu Tyr Leu Val Gly Ser Asp Gly Leu Ile Ser Phe Leu Glu	
280 285 290	
gtc aac acc cgc ctg cag gtg gag cac ccc gtc acc gag gag acc acc	1506
Val Asn Thr Arg Leu Gln Val Glu His Pro Val Thr Glu Glu Thr Thr	
295 300 305 310	
ggc atc gac ctg gtg cgc gag atg ttc cgc atc gcc gag ggc gcc gag	1554
Gly Ile Asp Leu Val Arg Glu Met Phe Arg Ile Ala Glu Gly Ala Glu	
315 320 325	
ctc tcc atc aag gag gac ccg acc cca cgc ggc cac gcc ttc gag ttc	1602
Leu Ser Ile Lys Glu Asp Pro Thr Pro Arg Gly His Ala Phe Glu Phe	
330 335 340	
cgc atc aac ggc gag gac gca ggc tcc aac ttc atg ccc gca ccg ggc	1650
Arg Ile Asn Gly Glu Asp Ala Gly Ser Asn Phe Met Pro Ala Pro Gly	
345 350 355	
aag atc acc cgc tac cgt gag ccc gcc ggc ccg ggt gtc cgc atg gac	1698
Lys Ile Thr Arg Tyr Arg Glu Pr Ala Gly Pro Gly Val Arg Met Asp	

特2000-12068

360	365	370	
tcc ggc gtt gtc gag ggt tcc gag atc tcc ggc cag ttc gac tcc atg 1746			
Ser Gly Val Val Glu Gly Ser Glu Ile Ser Gly Gln Phe Asp Ser Met			
375	380	385	390.
ctg gcc aag ctg atc gtc tgg ggc cag acc cgt gag cag gcc ctg gag 1794			
Leu Ala Lys Leu Ile Val Trp Gly Gln Thr Arg Glu Gln Ala Leu Glu			
395	400	405	
cgt tcc cgt cgt gcg ctc ggc gag tac atc gtc gag ggc atg ccg acc 1842			
Arg Ser Arg Arg Ala Leu Gly Glu Tyr Ile Val Glu Gly Met Pro Thr			
410	415	420	
gtc atc ccg ttc cac tcc cac atc gtc tcc aac ccg gca ttc gtc ggt 1890			
Val Ile Pro Phe His Ser His Ile Val Ser Asn Pro Ala Phe Val Gly			
425	430	435	
gac ggc gag ggc ttc gag gtc tac acc aag tgg atc gag gag gtc tgg 1938			
Asp Gly Glu Gly Phe Glu Val Tyr Thr Lys Trp Ile Glu Glu Val Trp			
440	445	450	
gac aac ccg atc gag ccg ttc gtc gat gca gcc gac ctc gac gac gag 1986			
Asp Asn Pro Ile Glu Pro Phe Val Asp Ala Ala Asp Leu Asp Asp Glu			
455	460	465	470
gag aag acc ccg tcg cag aag gtc atc gtc gag atc gac ggc cgc cgc 2034			
Glu Lys Thr Pro Ser Gln Lys Val Ile Val Glu Ile Asp Gly Arg Arg			
475	480	485	
gtc gag gtg gct ctc ccg ggc gac ctc gct ctc ggc ggt ggc gca ggt 2082			
Val Glu Val Ala Leu Pro Gly Asp Leu Ala Leu Gly Gly Ala Gly			
490	495	500	
gcc gcc aag aag aag ccg aag aag cgt cgc gca ggt ggc gcc aag gcc 2130			
Ala Ala Lys Lys Lys Pr Lys Lys Arg Arg Ala Gly Gly Ala Lys Ala			
505	510	515	
ggt gtc tcc ggt gac tcc gtc gca gcc ccg atg cag ggc acc gtc atc 2178			

Gly Val Ser Gly Asp Ser Val Ala Ala Pro Met Gln Gly Thr Val Ile
 520 525 530
 aag gtc aac gtt gag gac ggc gcc gag gtc tcc gag ggt gac acc gtc 2226
 Lys Val Asn Val Glu Asp Gly Ala Glu Val Ser Glu Gly Asp Thr Val
 535 540 545 550
 gtg gtt ctc gag gcc atg aag atg gag aac ccg gtc aag gcc cac aag 2274
 Val Val Leu Glu Ala Met Lys Met Glu Asn Pro Val Lys Ala His Lys
 555 560 565
 tcc ggt acc gtc tcc ggt ctg acc atc gcc gcg ggt gag ggc gtg acc 2322
 Ser Gly Thr Val Ser Gly Leu Thr Ile Ala Ala Gly Glu Gly Val Thr
 570 575 580
 aag ggt cag gtt ctc ctg gag atc aag taatcccttc aggaaacaga 2369
 -Lys Gly-Gln-Val-Leu-Leu-Glu-Ile-Lys-
 585 590
 cagccctgtt ct 2381

[0070]

<210> 4

<211> 591

<212> PRT

<213> *Corynebacterium thermoaminogenes*

<400> 4

Val Ser Val Glu Thr Arg Lys Ile Thr Lys Val Leu Val Ala Asn Arg
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 Gly Glu Ile Ala Ile Arg Val Phe Arg Ala Ala Arg Asp Glu Gly Ile
 20 25 30
 Ala Ser Val Ala Val Tyr Ala Glu Pro Asp Ala Asp Ala Pro Phe Val
 35 40 45
 Glu Tyr Ala Asp Glu Ala Phe Ala Leu Gly Gly Gln Thr Ser Ala Glu

50	55	60	
Ser Tyr Leu Val Ile Asp Lys Ile Ile Asp Ala Ala Arg Lys Ser Gly			
65	70	75	80
Ala Asp Ala Val His Pro Gly Tyr Gly Phe Leu Ala Glu Asn Ala Asp			
85	90	95	
Phe Ala Glu Ala Val Ile Asn Glu Gly Leu Ile Trp Ile Gly Pro Ser			—
100	105	110	
Pro Glu Ser Ile Arg Ser Leu Gly Asp Lys Val Thr Ala Arg His Ile			
115	120	125	
Ala Asn Asn Ala Asn Ala Pro Met Ala Pro Gly Thr Lys Glu Pro Val			
130	135	140	
Lys Asp Ala Ala Glu Val Val Ala Phe Ala Glu Glu Phe Gly Leu Pro			
145	150	155	160
Ile Ala Ile Lys Ala Ala Phe Gly Gly Gly Arg Gly Met Lys Val			
165	170	175	
Ala Tyr Glu Met Asp Glu Val Ala Asp Leu Phe Glu Ser Ala Thr Arg			
180	185	190	
Glu Ala Thr Ala Ala Phe Gly Arg Gly Glu Cys Phe Val Glu Arg Tyr			
195	200	205	
Leu Asp Lys Ala Arg His Val Glu Ala Gln Val Ile Ala Asp Lys His			
210	215	220	
Gly Asn Val Val Ala Gly Thr Arg Asp Cys Ser Leu Gln Arg Arg			
225	230	235	240
Phe Gln Lys Leu Val Glu Glu Ala Pro Ala Pro Phe Leu Thr Asp Glu			
245	250	255	
Gln Arg Asp Arg Ile His Ser Ser Ala Lys Ala Ile Cys Arg Glu Ala			
260	265	270	
Gly Tyr Tyr Gly Ala Gly Thr Val Glu Tyr Leu Val Gly Ser Asp Gly			
275	280	285	

Leu Ile Ser Phe Leu Glu Val Asn Thr Arg Leu Gln Val Glu His Pro
 290 295 300
 Val Thr Glu Glu Thr Thr Gly Ile Asp Leu Val Arg Glu Met Phe Arg
 305 310 315 320
 Ile Ala Glu Gly Ala Glu Leu Ser Ile Lys Glu Asp Pro Thr Pro Arg
 -325 -330 -335
 Gly His Ala Phe Glu Phe Arg Ile Asn Gly Glu Asp Ala Gly Ser Asn
 340 345 350
 Phe Met Pro Ala Pro Gly Lys Ile Thr Arg Tyr Arg Glu Pro Ala Gly
 355 360 365
 Pro Gly Val Arg Met Asp Ser Gly Val Val Glu Gly Ser Glu Ile Ser
 370 375 380
 Gly Gln Phe Asp Ser Met Leu Ala Lys Leu Ile Val Trp Gly Gln Thr
 385 390 395 400
 Arg Glu Gln Ala Leu Glu Arg Ser Arg Arg Ala Leu Gly Glu Tyr Ile
 405 410 415
 Val Glu Gly Met Pro Thr Val Ile Pro Phe His Ser His Ile Val Ser
 420 425 430
 Asn Pro Ala Phe Val Gly Asp Gly Glu Gly Phe Glu Val Tyr Thr Lys
 435 440 445
 Trp Ile Glu Glu Val Trp Asp Asn Pro Ile Glu Pro Phe Val Asp Ala
 450 455 460
 Ala Asp Leu Asp Asp Glu Glu Lys Thr Pro Ser Gln Lys Val Ile Val
 465 470 475 480
 Glu Ile Asp Gly Arg Arg Val Glu Val Ala Leu Pro Gly Asp Leu Ala
 485 490 495
 Leu Gly Gly Ala Gly Ala Ala Lys Lys Lys Pr Lys Lys Arg Arg
 500 505 510
 Ala Gly Gly Ala Lys Ala Gly Val Ser Gly Asp Ser Val Ala Ala Pr

515	520	525
Met Gln Gly Thr Val Ile Lys Val Asn Val Glu Asp Gly Ala Glu Val		
530	535	540
Ser Glu Gly Asp Thr Val Val Val Leu Glu Ala Met Lys Met Glu Asn		
545	550	555
-Pro-Val-Lys-Ala-His-Lys-Ser-Gly-Thr-Val-Ser-Gly-Leu-Thr-Ile-Ala		
565	570	575
Ala Gly Glu Gly Val Thr Lys Gly Gln Val Leu Leu Glu Ile Lys		
580	585	590

[0071]

<210> 5

<211> 2128

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (339)..(1967)

<400> 5

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atccacactgt ggaacagtca gcggcgcggc catggagggc agcgacaggt gacgtccgag 180
cacccggttc cccaccgtgg acacggcatt gatccgacac ggtggggata gtttcatgct 240
gaaaaactat cgctgtgcag ggaggatccg gaatgtgacc tatttcatgg agaaatgatt 300
gtggacgata ccccccggta cggctaccat tccaaaac atg acc att tcc tca cct 356

```

Met Thr Ile Ser Ser Pr

1

5

ttg att gac gtc gct aac ctg cca gac atc aac acc acc ggc aag 404

Leu Ile Asp Val Ala Asn Leu Pro Asp Ile Asn Thr Thr Ala Gly Lys
 10 15 20
 atc gcc gac ctg aag gcc cgc cg^g gaa gac cac ttc ccc atg ggt 452
 Ile Ala Asp Leu Lys Ala Arg Arg Ala Glu Ala His Phe Pro Met Gly
 25 30 35
 -gaa-aag-gcc-gta-gag-aag-gtc-cac-gcg-gcc-aac-cgc-ctc-acc-gcg-cgc 500
 Glu Lys Ala Val Glu Lys Val His Ala Ala Asn Arg Leu Thr Ala Arg
 40 45 50
 gaa cga ctt gac tac ctg ctc gat gaa ggc tcc ttc atc gaa acc gat 548
 Glu Arg Leu Asp Tyr Leu Leu Asp Glu Gly Ser Phe Ile Glu Thr Asp
 55 60 65 70
 cag ctc gca cgc cac cgc acc acc gc^g ttc ggc ctg ggc aac aag cga 596
 Gln Leu Ala Arg His Arg Thr Thr Ala Phe Gly Leu Gly Asn Lys Arg
 75 80 85
 ccg gcc acc gac ggc atc gtc acc ggc tgg ggc acc atc gac ggc cgc 644
 Pro Ala Thr Asp Gly Ile Val Thr Gly Trp Gly Thr Ile Asp Gly Arg
 90 95 100
 gag gtc tgc atc ttc tcc cag gac ggc acc gtc ttc ggt ggc gca ctc 692
 Glu Val Cys Ile Phe Ser Gln Asp Gly Thr Val Phe Gly Gly Ala Leu
 105 110 115
 ggt gag gtc tac ggc gag aag atg atc aag atc atg gag ctg gcc atc 740
 Gly Glu Val Tyr Gly Glu Lys Met Ile Lys Ile Met Glu Leu Ala Ile
 120 125 130
 gac acc ggc cgc cca ctc atc ggc ctg tac gag ggt gca ggt gcc cgc 788
 Asp Thr Gly Arg Pro Leu Ile Gly Leu Tyr Glu Gly Ala Gly Ala Arg
 135 140 145 150
 atc cag gac ggt gcg gtc tcc ctc gac ttc atc tcc cag acc ttc tat 836
 Ile Gln Asp Gly Ala Val Ser Leu Asp Phe Ile Ser Gln Thr Phe Tyr
 155 160 165

cag aac atc cag gcc tcc ggc gtg atc ccg cag atc tcc gtg atc atg			884
Gln Asn Ile Gln Ala Ser Gly Val Ile Pro Gln Ile Ser Val Ile Met			
170	175	180	
ggt gcc tgc gcc ggt ggc aac gcc tac ggc ccg gcc ctg acc gac ttc			932
Gly Ala Cys Ala Gly Gly Asn Ala Tyr Gly Pro Ala Leu Thr Asp Phe			
185	190	195	
gtg gtc atg gtg gac aag acc tcg aag atg ttc gtc acc ggc ccc gat			980
Val Val Met Val Asp Lys Thr Ser Lys Met Phe Val Thr Gly Pro Asp			
200	205	210	
gtg atc aag acc gtc acc ggc gag gag atc acc cag gag gag ctc ggc			1028
Val Ile Lys Thr Val Thr Gly Glu Glu Ile Thr Gln Glu Glu Leu Gly			
215	220	225	230
gga gca acc acc cac atg gtc acc gcc ggc aac tcc cac tac acc gtc			1076
Gly Ala Thr Thr His Met Val Thr Ala Gly Asn Ser His Tyr Thr Val			
235	240	245	
gcc acc gat gag gag gcc ctc gac tgg gtc cag gac ctc atc tcc ttc			1124
Ala Thr Asp Glu Glu Ala Leu Asp Trp Val Gln Asp Leu Ile Ser Phe			
250	255	260	
ctg ccc tcc aac aat cgc tcc tac gcc ccg gtg gag gag ttc gac gag			1172
Leu Pro Ser Asn Asn Arg Ser Tyr Ala Pro Val Glu Glu Phe Asp Glu			
265	270	275	
gag gac ggt ggc atc gcc gag aac atc acc gcc gat gac ctg aag ctg			1220
Glu Asp Gly Gly Ile Ala Glu Asn Ile Thr Ala Asp Asp Leu Lys Leu			
280	285	290	
gat gag atc atc ccg gat tcc gcc acc gtg ccc tat gat gtc cgc gac			1268
Asp Glu Ile Ile Pro Asp Ser Ala Thr Val Pro Tyr Asp Val Arg Asp			
295	300	305	310
gtc atc cag tgc ctg acc gac gac ggt gag tac ctg gag atc cag gcc			1316
Val Ile Gln Cys Leu Thr Asp Asp Gly Glu Tyr Leu Glu Ile Gln Ala			

315	320	325	
gac cga gcc gag aat gtc gtc atc gcc ttc ggc cgc atc gag ggc cag 1364			
Asp Arg Ala Glu Asn Val Val Ile Ala Phe Gly Arg Ile Glu Gly Gln			
330	335	340	
tcc gtc ggt ttc gtc gcc aac cag ccg acc cag ttc gcc ggc tgc ctg 1412			
Ser Val Gly Phe Val Ala Asn Gln Pro Thr Gln-Phe-Ala-Gly Cys Leu			
345	350	355	
gac atc gac tcc tcc gag aag gca gcc cgc ttc gtc cgc acc tgc gat 1460			
Asp Ile Asp Ser Ser Glu Lys Ala Ala Arg Phe Val Arg Thr Cys Asp			
360	365	370	
gcc ttc aac atc ccg atc gtc atg ctt gtc gac gtc ccc ggc ttc ctc 1508			
Ala Phe Asn Ile Pro Ile Val Met Leu Val Asp Val Pro Gly Phe Leu			
375	380	385	390
ccc ggt gcc ggc cag gag tac ggc ggc atc ctg cgt cgt ggc gcc aaa 1556			
Pro Gly Ala Gly Gln Glu Tyr Gly Gly Ile Leu Arg Arg Gly Ala Lys			
395	400	405	
ctg ctc tac gcc tac ggt gag gcc acc gtc ccg aag atc acc gtg acc 1604			
Leu Leu Tyr Ala Tyr Gly Glu Ala Thr Val Pro Lys Ile Thr Val Thr			
410	415	420	
atg cgc aag gcc tac ggc ggt gcg tac tgt gtc atg gga tcc aag ggt 1652			
Met Arg Lys Ala Tyr Gly Ala Tyr Cys Val Met Gly Ser Lys Gly			
425	430	435	
ctg ggc gca gac atc aac ctg gcc tgg ccg acc gcg cag atc gcc gtc 1700			
Leu Gly Ala Asp Ile Asn Leu Ala Trp Pro Thr Ala Gln Ile Ala Val			
440	445	450	
atg ggt gcc ggc ggc gtc cag ttc atc tac cgc aag gag ctc atg 1748			
Met Gly Ala Ala Gly Ala Val Gln Phe Ile Tyr Arg Lys Glu Leu Met			
455	460	465	470
gcc gct gat gcc aag ggc ctg gac acc gtc gcc ctg gcc cag tcc ttc 1796			

Ala Ala Asp Ala Lys Gly Leu Asp Thr Val Ala Leu Ala Gln Ser Phe
 475 480 485
 gag cgt gag tac gag gac cac atg ctc aac ccg tac ctg gcg gcc gag 1844
 Glu Arg Glu Tyr Glu Asp His Met Leu Asn Pro Tyr Leu Ala Ala Glu
 490 495 500
 cgt ggc ctc atc gac gcg gtg atc ctg ccg tcc gag acc cgt ggc cag 1892
 Arg Gly Leu Ile Asp Ala Val Ile Leu Pro Ser Glu Thr Arg Gly Gln
 505 510 515
 atc gca cgc aac ctg cgt ctg aag cac aag aat gtc tcc cgc cct 1940
 Ile Ala Arg Asn Leu Arg Leu Leu Lys His Lys Asn Val Ser Arg Pro
 520 525 530
 gcc cgc aag cac ggc aac atg cca ctg taagcacccg ggaccacccc 1987
 Ala Arg Lys His Gly Asn Met Pro Leu
 535 540
 ctacgccccgc acccacggcc ctttgctggc aggtgcggc gctgtgcgtt ttccgcgcct 2047
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[0072]

<210> 6

<211> 543

<212> PRT

<213> *Corynebacterium thermoaminogenes*

<400> 6

Met Thr Ile Ser Ser Pro Leu Ile Asp Val Ala Asn Leu Pro Asp Ile
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Asn Thr Thr Ala Gly Lys Ile Ala Asp Leu Lys Ala Arg Arg Ala Glu
 20 25 30

Ala His Phe Pr Met Gly Glu Lys Ala Val Glu Lys Val His Ala Ala

35	40	45
Asn Arg Leu Thr Ala Arg Glu Arg Leu Asp Tyr Leu Leu Asp Glu Gly		
50	55	60
Ser Phe Ile Glu Thr Asp Gln Leu Ala Arg His Arg Thr Thr Ala Phe		
65	70	75
Gly Leu Gly Asn Lys Arg Pro Ala Thr Asp Gly Ile Val Thr Gly Trp		
85	90	95
Gly Thr Ile Asp Gly Arg Glu Val Cys Ile Phe Ser Gln Asp Gly Thr		
100	105	110
Val Phe Gly Gly Ala Leu Gly Glu Val Tyr Gly Glu Lys Met Ile Lys		
115	120	125
Ile Met Glu Leu Ala Ile Asp Thr Gly Arg Pro Leu Ile Gly Leu Tyr		
130	135	140
Glu Gly Ala Gly Ala Arg Ile Gln Asp Gly Ala Val Ser Leu Asp Phe		
145	150	155
Ile Ser Gln Thr Phe Tyr Gln Asn Ile Gln Ala Ser Gly Val Ile Pro		
165	170	175
Gln Ile Ser Val Ile Met Gly Ala Cys Ala Gly Gly Asn Ala Tyr Gly		
180	185	190
Pro Ala Leu Thr Asp Phe Val Val Met Val Asp Lys Thr Ser Lys Met		
195	200	205
Phe Val Thr Gly Pro Asp Val Ile Lys Thr Val Thr Gly Glu Glu Ile		
210	215	220
Thr Gln Glu Glu Leu Gly Ala Thr Thr His Met Val Thr Ala Gly		
225	230	235
Asn Ser His Tyr Thr Val Ala Thr Asp Glu Glu Ala Leu Asp Trp Val		
245	250	255
Gln Asp Leu Ile Ser Phe Leu Pro Ser Asn Asn Arg Ser Tyr Ala Pro		
260	265	270

Val Glu Glu Phe Asp Glu Glu Asp Gly Gly Ile Ala Glu Asn Ile Thr
 275 280 285
 Ala Asp Asp Leu Lys Leu Asp Glu Ile Ile Pro Asp Ser Ala Thr Val
 290 295 300
 Pro Tyr Asp Val Arg Asp Val Ile Gln Cys Leu Thr Asp Asp Gly Glu
 305 --- 310 --- 315 --- 320
 Tyr Leu Glu Ile Gln Ala Asp Arg Ala Glu Asn Val Val Ile Ala Phe
 325 330 335
 Gly Arg Ile Glu Gly Gln Ser Val Gly Phe Val Ala Asn Gln Pro Thr
 340 345 350
 Gln Phe Ala Gly Cys Leu Asp Ile Asp Ser Ser Glu Lys Ala Ala Arg
 355 360 365
 Phe Val Arg Thr Cys Asp Ala Phe Asn Ile Pro Ile Val Met Leu Val
 370 375 380
 Asp Val Pro Gly Phe Leu Pro Gly Ala Gly Gln Glu Tyr Gly Ile
 385 390 395 400
 Leu Arg Arg Gly Ala Lys Leu Leu Tyr Ala Tyr Gly Glu Ala Thr Val
 405 410 415
 Pro Lys Ile Thr Val Thr Met Arg Lys Ala Tyr Gly Ala Tyr Cys
 420 425 430
 Val Met Gly Ser Lys Gly Leu Gly Ala Asp Ile Asn Leu Ala Trp Pro
 435 440 445
 Thr Ala Gln Ile Ala Val Met Gly Ala Ala Gly Ala Val Gln Phe Ile
 450 455 460
 Tyr Arg Lys Glu Leu Met Ala Ala Asp Ala Lys Gly Leu Asp Thr Val
 465 470 475 480
 Ala Leu Ala Gln Ser Phe Glu Arg Glu Tyr Glu Asp His Met Leu Asn
 485 490 495
 Pro Tyr Leu Ala Ala Glu Arg Gly Leu Ile Asp Ala Val Ile Leu Pro

500	505	510
Ser Glu Thr Arg Gly Gln Ile Ala Arg Asn Leu Arg L u L u Lys His		
515	520	525
Lys Asn Val Ser Arg Pro Ala Arg Lys His Gly Asn Met Pro Leu		
530	535	540

—[0-0-7-3]—

<210> 7
<211> 2076
<212> DNA
<213> **Corynebacterium thermoaminogenes**

<220>
<221> CDS
<222> (412)..(2022)

<400> 7

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acggggggga ggaggtcaca taggccatac gctgcacttt tgatgaagtg tgggcagatc 180
gaccgggcaa atctggaaa taaggggcct ggtgaactag cattccctt agcgaagggt 240
gagcatcgcg gaccccgca tgcccaacc ggtcgtaaat tcatgtgccg ccacagtccc 300
ctcaccaggg gatcggaacc agcccagcct gattccggcg tgacggacct caccgtgaac 360
aagtccccgc attactcaca gaactcacac caggatitag actaagaaac c atg act 417
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Met Thr

1

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gca gca acg aca gca cct gat ctg acc acc acc gcc ggc aaa ctc gcg 465
Ala Ala Thr Thr Ala Pro Asp Leu Thr Thr Ala Gly Lys Leu Ala
5 10 15
gat ctc cgc gcc cgc ctt tcc gag acc cag gcc ccc atg ggt cag gcc 513
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Asp Leu Arg Ala Arg Leu Ser Glu Thr Gln Ala Pro Met Gly Gln Ala
 20 25 30
 tcc gtg gag aag gtg cac gag gca ggg aag aag acc gca cgc gag cgc 561
 Ser Val Glu Lys Val His Glu Ala Gly Lys Lys Thr Ala Arg Glu Arg
 35 40 45 50
 atc gag tac ctg ctc gat gag ggc tcc ttc gtt gag gtc gat gcc ctc 609
 Ile Glu Tyr Leu Leu Asp Glu Gly Ser Phe Val Glu Val Asp Ala Leu
 55 60 65
 gcc cgc cac cgt tcc aag aac ttc ggc ctg gac tcc aag cgc ccg gtc 657
 Ala Arg His Arg Ser Lys Asn Phe Gly Leu Asp Ser Lys Arg Pro Val
 70 75 80
 acc gac ggt gtg gtc acc ggt tac ggc acc atc gac gga cgc aag gtc 705
 Thr Asp Gly Val Val Thr Gly Tyr Gly Thr Ile Asp Gly Arg Lys Val
 85 90 95
 tgc gtc ttc tcc cag gac ggc gct atc ttc ggc ggt gcc ctc ggt gag 753
 Cys Val Phe Ser Gln Asp Gly Ala Ile Phe Gly Gly Ala Leu Gly Glu
 100 105 110
 gtc tac ggc gag aag atc gtc aag atc atg gac ctg gcc atc aag acc 801
 Val Tyr Gly Glu Lys Ile Val Lys Ile Met Asp Leu Ala Ile Lys Thr
 115 120 125 130
 ggt gtc ccc ctc atc ggc atc aac gag ggc gcc ggc cgc atc cag 849
 Gly Val Pro Leu Ile Gly Ile Asn Glu Gly Ala Gly Ala Arg Ile Gln
 135 140 145
 gaa ggc gtt gtc tcc ctg ggc ctg tac tcc cag atc ttc tac cgc aac 897
 Glu Gly Val Val Ser Leu Gly Leu Tyr Ser Gln Ile Phe Tyr Arg Asn
 150 155 160
 acc cag gca tcc ggt gtc atc cca cag atc tcc ctc atc atg ggt gcc 945
 Thr Gln Ala Ser Gly Val Ile Pr Gln Ile Ser Leu Ile Met Gly Ala
 165 170 175

tgc gcc ggt ggc cat gtg tac tcc ccc gcc ctg acc gac ttc atc atc 993
 Cys Ala Gly Gly His Val Tyr Ser Pro Ala Leu Thr Asp Phe Ile Ile
 180 185 190
 atg gtg gac aag acc tcc aag atg ttc atc acc ggc ccc gac gtc atc 1041
 Met Val Asp Lys Thr Ser Lys Met Phe Ile Thr Gly Pro Asp Val Ile
 195 200 205 210
 aag acc gtc acc ggc gag gag gtc acc cag gag gaa ctg ggt ggc 1089
 Lys Thr Val Thr Gly Glu Glu Val Thr Gln Glu Glu Leu Gly Ala
 215 220 225
 tac acc cac atg gcc cag tcc ggc acc tcg cac tac acc gca gcc gat 1137
 Tyr Thr His Met Ala Gln Ser Gly Thr Ser His Tyr Thr Ala Ala Asp
 230 235 240
 gac tcc gat gcc ctc gac tgg gtc cgt gag ctg gtc agc tac ctg ccg 1185
 Asp Ser Asp Ala Leu Asp Trp Val Arg Glu Leu Val Ser Tyr Leu Pro
 245 250 255
 tcc aac aac cgt gcg gag acc cca cgc cag gac gcc gac atc atg gtg 1233
 Ser Asn Asn Arg Ala Glu Thr Pro Arg Gln Asp Ala Asp Ile Met Val
 260 265 270
 ggc tcc atc aag gag aac atc acc gag acc gac ctc gaa ctc gac acc 1281
 Gly Ser Ile Lys Glu Asn Ile Thr Glu Thr Asp Leu Glu Leu Asp Thr
 275 280 285 290
 ctg atc ccg gat tcc ccg aac cag ccg tac gac atg aag gac gtc atc 1329
 Leu Ile Pro Asp Ser Pro Asn Gln Pro Tyr Asp Met Lys Asp Val Ile
 295 300 305
 acc cgc atc gtc gat gat gcc gag ttc ttc gag atc cag gag ggt tac 1377
 Thr Arg Ile Val Asp Asp Ala Glu Phe Phe Glu Ile Gln Glu Gly Tyr
 310 315 320
 gcc gag aac atc atc tgc ggt ttc gcc cgc gtc gag ggt cgt gcc gtg 1425
 Ala Glu Asn Ile Ile Cys Gly Phe Ala Arg Val Glu Gly Arg Ala Val

325	330	335	
ggt atc gtg gcc aac cag ccg atg cag ttc gcc ggc tgc ctg gac atc 1473			
Gly Ile Val Ala Asn Gln Pro Met Gln Phe Ala Gly Cys Leu Asp Ile			
340	345	350	
aag gca tcc gag aag gcc gcc cgc ttc atc cgc acc tgt gac gcc ttc 1521			
Lys Ala Ser Glu Lys Ala Ala Arg Phe Ile Arg Thr Cys Asp Ala Phe			
355	360	365	370
aac atc ccg atc atc gag ctt gtc gac gtc cca ggc ttc ctc ccg ggc 1569			
Asn Ile Pro Ile Ile Glu Leu Val Asp Val Pro Gly Phe Leu Pro Gly			
375	380	385	
acc aac cag gag ttc gac ggc atc atc cgt cgc ggc gcg aag ctg ctc 1617			
Thr Asn Gln Glu Phe Asp Gly Ile Ile Arg Arg Gly Ala Lys Leu Leu			
390	395	400	
tac gcc tac gcc gag gcc acc gtc ggc aag atc acc gtg atc acc cgc 1665			
Tyr Ala Tyr Ala Glu Ala Thr Val Gly Lys Ile Thr Val Ile Thr Arg			
405	410	415	
aag tcc tac ggc ggt gcc tac tgc gtg atg ggc tcc aag gac atg ggt 1713			
Lys Ser Tyr Gly Ala Tyr Cys Val Met Gly Ser Lys Asp Met Gly			
420	425	430	
gcg gac ctc gtc ttc gca tgg ccc acc gcg cag atc gcc gtc atg ggt 1761			
Ala Asp Leu Val Phe Ala Trp Pro Thr Ala Gln Ile Ala Val Met Gly			
435	440	445	450
gcc tcc ggt gcc gtc ggc ttc atc tac cgc aag gag ctc aag cag gct 1809			
Ala Ser Gly Ala Val Gly Phe Ile Tyr Arg Lys Glu Leu Lys Gln Ala			
455	460	465	
gca gcg gcc ggc gag gat gtc acc gcg ctg atg aag aag tac gag cag 1857			
Ala Ala Ala Gly Glu Asp Val Thr Ala Leu Met Lys Lys Tyr Glu Gln			
470	475	480	
gag tac gag gag acc ctg gtc aac ccg tac atg gct gca gag cgt ggc 1905			

Glu Tyr Glu Glu Thr Leu Val Asn Pro Tyr Met Ala Ala Glu Arg Gly

485

490

495

tac gtc gac gcc gtc atc cca cca tcc gag acc cgt ggt cag atc atc 1953

Tyr Val Asp Ala Val Ile Pro Pro Ser Glu Thr Arg Gly Gln Ile Ile

500

505

510

-gag-ggt-ctg-cgt-ctg-ctc-gac-cgc-aag-gtg-gtc-aac-gtc-ccg-gcc aag -2001

Glu Gly Leu Arg Leu Leu Asp Arg Lys Val Val Asn Val Pro Ala Lys

515

520

525

530

aag cac ggt aac atc ccg ctg taaaccgtct tccccctccgg caccacgccc 2052

Lys His Gly Asn Ile Pro Leu

535

gagaaggctt tgtccgcagc tgtc 2076

[0074]

<210> 8

<211> 537

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 8

Met Thr Ala Ala Thr Thr Ala Pro Asp Leu Thr Thr Thr Ala Gly Lys

1

5

10

15

Leu Ala Asp Leu Arg Ala Arg Leu Ser Glu Thr Gln Ala Pro Met Gly

20

25

30

Gln Ala Ser Val Glu Lys Val His Glu Ala Gly Lys Lys Thr Ala Arg

35

40

45

Glu Arg Ile Glu Tyr Leu Leu Asp Glu Gly Ser Phe Val Glu Val Asp

50

55

60

Ala Leu Ala Arg His Arg Ser Lys Asn Phe Gly Leu Asp Ser Lys Arg

65

70

75

80

Pro Val Thr Asp Gly Val Val Thr Gly Tyr Gly Thr Ile Asp Gly Arg
 85 90 95
 Lys Val Cys Val Phe Ser Gln Asp Gly Ala Ile Phe Gly Gly Ala Leu
 100 105 110
 Gly Glu Val Tyr Gly Glu Lys Ile Val Lys Ile Met Asp Leu Ala Ile
 115 120 125
 Lys Thr Gly Val Pro Leu Ile Gly Ile Asn Glu Gly Ala Gly Ala Arg
 130 135 140
 Ile Gln Glu Gly Val Val Ser Leu Gly Leu Tyr Ser Gln Ile Phe Tyr
 145 150 155 160
 Arg Asn Thr Gln Ala Ser Gly Val Ile Pro Gln Ile Ser Leu Ile Met
 165 170 175
 Gly Ala Cys Ala Gly Gly His Val Tyr Ser Pro Ala Leu Thr Asp Phe
 180 185 190
 Ile Ile Met Val Asp Lys Thr Ser Lys Met Phe Ile Thr Gly Pro Asp
 195 200 205
 Val Ile Lys Thr Val Thr Gly Glu Glu Val Thr Gln Glu Glu Leu Gly
 210 215 220
 Gly Ala Tyr Thr His Met Ala Gln Ser Gly Thr Ser His Tyr Thr Ala
 225 230 235 240
 Ala Asp Asp Ser Asp Ala Leu Asp Trp Val Arg Glu Leu Val Ser Tyr
 245 250 255
 Leu Pro Ser Asn Asn Arg Ala Glu Thr Pro Arg Gln Asp Ala Asp Ile
 260 265 270
 Met Val Gly Ser Ile Lys Glu Asn Ile Thr Glu Thr Asp Leu Glu Leu
 275 280 285
 Asp Thr Leu Ile Pro Asp Ser Pr Asn Gln Pr Tyr Asp Met Lys Asp
 290 295 300
 Val Ile Thr Arg Ile Val Asp Asp Ala Glu Phe Phe Glu Ile Gln Glu

305	310	315	320
Gly Tyr Ala Glu Asn Ile Ile Cys Gly Phe Ala Arg Val Glu Gly Arg			
325	330	335	
Ala Val Gly Ile Val Ala Asn Gln Pro Met Gln Phe Ala Gly Cys Leu			
340	345	350	
Asp Ile Lys Ala Ser Glu Lys Ala Ala Arg Phe Ile Arg Thr Cys Asp			
355	360	365	
Ala Phe Asn Ile Pro Ile Ile Glu Leu Val Asp Val Pro Gly Phe Leu			
370	375	380	
Pro Gly Thr Asn Gln Glu Phe Asp Gly Ile Ile Arg Arg Gly Ala Lys			
385	390	395	400
Leu Leu Tyr Ala Tyr Ala Glu Ala Thr Val Gly Lys Ile Thr Val Ile			
405	410	415	
Thr Arg Lys Ser Tyr Gly Gly Ala Tyr Cys Val Met Gly Ser Lys Asp			
420	425	430	
Met Gly Ala Asp Leu Val Phe Ala Trp Pro Thr Ala Gln Ile Ala Val			
435	440	445	
Met Gly Ala Ser Gly Ala Val Gly Phe Ile Tyr Arg Lys Glu Leu Lys			
450	455	460	
Gln Ala Ala Ala Ala Gly Glu Asp Val Thr Ala Leu Met Lys Lys Tyr			
465	470	475	480
Glu Gln Glu Tyr Glu Glu Thr Leu Val Asn Pro Tyr Met Ala Ala Glu			
485	490	495	
Arg Gly Tyr Val Asp Ala Val Ile Pro Pro Ser Glu Thr Arg Gly Gln			
500	505	510	
Ile Ile Glu Gly Leu Arg Leu Leu Asp Arg Lys Val Val Asn Val Pro			
515	520	525	
Ala Lys Lys His Gly Asn Ile Pr Leu			
530	535		

【0075】

<210> 9

<211> 1643

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (326)..(1363)

<400> 9

agcgcgccgg cagccaccag tgggatcggt cccagcggac ggatgccggga ttcacggcgg 60
 tcagccaccc gccgatgaga cctgcagcga caacggtggc ggtgctgacc tggtcagcgt 120
 ctttagttt catatccatg tcagacagtc taaccactct ctccgacgcg tccgaacatg 180
 ctggggtggc ggacaccatg tccgttcggg cgttgccccg acggggaaaa atgcaggca 240
 gatgtgtccg atgtggata aacccaccgg ttccggcgtg tcttcggat caatggcaca 300
 gcattaaaccg tgtgggggt ttaat atg gga gcc atg cga att gcc act ctc 352

Met Gly Ala Met Arg Ile Ala Thr Leu

1 5

acg tca ggc ggc gac tgc ccc gga ctc aat gct gtc atc agg gga atc 400

Thr Ser Gly Gly Asp Cys Pro Gly Leu Asn Ala Val Ile Arg Gly Ile

10 15 20 25

gtc cgt acc gca agt aat gaa ttc ggt tcc acc gtc gtg ggt tat cag 448

Val Arg Thr Ala Ser Asn Glu Phe Gly Ser Thr Val Val Gly Tyr Gln

30 35 40

gac ggc tgg gag ggc ctg ctg gcg gac cga cgt gtt cag ctc tat gac 496

Asp Gly Trp Glu Gly Leu Leu Ala Asp Arg Arg Val Gln Leu Tyr Asp

45 50 55

gat gag gac atc gac cgc atc ctg ctc cgc ggt gga aca atc ctg ggc 544

Asp Glu Asp Ile Asp Arg Ile Leu Leu Arg Gly Gly Thr Ile Leu Gly

60

65

70

acc ggt cgt ctc cac ccc gac aag ttc aga gcc gga atc gac cag gtc 592

Thr Gly Arg Leu His Pro Asp Lys Phe Arg Ala Gly Ile Asp Gln Val

75

80

85

aag-gcg-aat-ctc-gcc-gat-geg-gga-att-gac-gea-ctc-atc-ccg-atc-ggt 640

Lys Ala Asn Leu Ala Asp Ala Gly Ile Asp Ala Leu Ile Pro Ile Gly

90

95

100

105

ggc gag ggc acc ctc aag gga gcg aag tgg ctc gcc gac aac ggc atc 688

Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp Leu Ala Asp Asn Gly Ile

110

115

120

ccc gtg gtc ggt gtc ccg aaa acc atc gac aat gat gtc aac ggc acg 736

Pro Val Val Gly Val Pro Lys Thr Ile Asp Asn Asp Val Asn Gly Thr

125

130

135

gat ttc acc ttc ggt ttc gat tcc gcg gtc tct gtg gcc acc gac gcc 784

Asp Phe Thr Phe Gly Phe Asp Ser Ala Val Ser Val Ala Thr Asp Ala

140

145

150

atc gac cgg ctg cac acc acg gcg gaa tcc cac aac cgt gtg atg atc 832

Ile Asp Arg Leu His Thr Thr Ala Glu Ser His Asn Arg Val Met Ile

155

160

165

gtc gag gtc atg ggc cgc cac gtc ggt tgg atc gca ctg cat gcc ggc 880

Val Glu Val Met Gly Arg His Val Gly Trp Ile Ala Leu His Ala Gly

170

175

180

185

atg gcc ggt gga gcc cac tac acc gtc atc ccc gag gtg ccc ttc gac 928

Met Ala Gly Gly Ala His Tyr Thr Val Ile Pro Glu Val Pro Phe Asp

190

195

200

atc tcg gag atc tgc aag cgt atg gaa cgt cgc ttc cag atg ggg gag 976

Ile Ser Glu Ile Cys Lys Arg Met Glu Arg Arg Phe Gln Met Gly Glu

205

210

215

aag tac ggc atc atc gtc gtc gcg gag ggt gcc ctg ccc aag gag gga 1024
 Lys Tyr Gly Ile Ile Val Val Ala Glu Gly Ala Leu Pro Lys Glu Gly
 220 225 230
 acc atg gag ctg cgt gag ggg gag gtg gat cag ttc ggt cac aag acc 1072
 Thr Met Glu Leu Arg Glu Gly Glu Val Asp Gln Phe Gly His Lys Thr
 235 240 245 ..
 ttc acc ggc atc ggc cag cag atc gcc gac gag gtg cac agg cgt ctg 1120
 Phe Thr Gly Ile Gly Gln Gln Ile Ala Asp Glu Val His Arg Arg Leu
 250 255 260 265
 ggt cat gat gtc cgc acc acg gtc ctg ggc cat atc cag cgt ggt ggc 1168
 Gly His Asp Val Arg Thr Thr Val Leu Gly His Ile Gln Arg Gly Gly
 270 275 280
 acc ccc acc gcc ttc gac cgt gtc ctg gcc acc cgg tac ggt gtc cgc 1216
 Thr Pro Thr Ala Phe Asp Arg Val Leu Ala Thr Arg Tyr Gly Val Arg
 285 290 295
 gcc gcg cgt gcc tgc cac gag ggt cag ttc aac acc gtc gcg ctc 1264
 Ala Ala Arg Ala Cys His Glu Gly Gln Phe Asn Thr Val Val Ala Leu
 300 305 310
 aag ggg gag cgc atc cgg atg atc tcc ttc gat gag gcc gtg ggc acc 1312
 Lys Gly Glu Arg Ile Arg Met Ile Ser Phe Asp Glu Ala Val Gly Thr
 315 320 325
 ctg aag aag gtg ccg atg gaa cgc tgg gtg acc gcc cag gct atg ttc 1360
 Leu Lys Lys Val Pro Met Glu Arg Trp Val Thr Ala Gln Ala Met Phe
 330 335 340 345
 ggt tagtcaggcc gcattccgg ttccgcgcc gcggggccgg gtttttcat 1413
 Gly
 gccccggaac acatcggtat gaaatcgtga tatgcattac ttgacgggaa agtggggat 1473
 ccgtcacctc gcgttgtcca actacagccc gcagcgcctg cggaaattct tcgagcaatc 1533
 cgccgattcc ccggcccgtc ccgtcgccgt ccaaccgcag tacaatctgc tggcccgccg 1593

ggattatgag accggtatcc gcccggtcgt ggacgagttc ggtcccgccg 1643

【0076】

<210> 10

<211> 346

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 10

Met Gly Ala Met Arg Ile Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro

1

5

10

15

Gly Leu Asn Ala Val Ile Arg Gly Ile Val Arg Thr Ala Ser Asn Glu

20

25

30

Phe Gly Ser Thr Val Val-Gly-Tyr Gln-Asp Gly-Trp Glu-Gly-Leu Leu

35

40

45

Ala Asp Arg Arg Val Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile

50

55

60

Leu Leu Arg Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp

65

70

75

80

Lys Phe Arg Ala Gly Ile Asp Gln Val Lys Ala Asn Leu Ala Asp Ala

85

90

95

Gly Ile Asp Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly

100

105

110

Ala Lys Trp Leu Ala Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys

115

120

125

Thr Ile Asp Asn Asp Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp

130

135

140

Ser Ala Val Ser Val Ala Thr Asp Ala Ile Asp Arg Leu His Thr Thr

145

150

155

160

Ala Glu Ser His Asn Arg Val Met Ile Val Glu Val Met Gly Arg His

165	170	175
Val Gly Trp Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr		
180	185	190
Thr Val Ile Pro Glu Val Pro Phe Asp Ile Ser Glu Ile Cys Lys Arg		
195	200	205
Met Glu Arg Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val		
210	215	220
Ala Glu Gly Ala Leu Pro Lys Glu Gly Thr Met Glu Leu Arg Glu Gly		
225	230	235
Glu Val Asp Gln Phe Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln		
245	250	255
Ile Ala Asp Glu Val His Arg Arg Leu Gly His Asp Val Arg Thr Thr		
260	265	270
Val Leu Gly His Ile Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg		
275	280	285
Val Leu Ala Thr Arg Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu		
290	295	300
Gly Gln Phe Asn Thr Val Val Ala Leu Lys Gly Glu Arg Ile Arg Met		
305	310	315
Ile Ser Phe Asp Glu Ala Val Gly Thr Leu Lys Lys Val Pro Met Glu		
325	330	335
Arg Trp Val Thr Ala Gln Ala Met Phe Gly		
340	345	

【0077】

<210> 11

<211> 498

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (1)..(498)

<400> 11

tac tac cag cac gat cca ggt ttc ccc ttc gca cca aag cgc acc ggt	48
Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly	
1 5 10 15	
ggg tct cac acc acc acg ccg ttg acc gga ccg cag cga ttg cag tgg	96
Trp Ala His Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp	
20 25 30	
acg cac ctg ccc gat gct ctt tac ccg gat gta tcc tat gac ctg gat	144
Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Val Ser Tyr Asp Leu Asp	
35 40 45	
gga tgc tat tcc ggc gga gcc gta ttt tct gac ggc acg ctt aaa ctt	192
Gly Cys Tyr Ser Gly Gly Ala Val Phe Ser Asp Gly Thr Leu Lys Leu	
50 55 60	
ttc tac acc ggc aac cga aaa att gac ggc aag cgc cgc gcc acc caa	240
Phe Tyr Thr Gly Asn Arg Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln	
65 70 75 80	
aac ctc gtc gaa gtc gag gac cca act ggg ctg atg ggc ggc att cat	288
Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His	
85 90 95	
cgc cgc tcg cct aaa aat ccg ctt atc gac gga ccc gcc agc ggt ttt	336
Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe	
100 105 110	
acg ccc cac tac cgc gat ccc atg atc agc cct gat ggg gat ggt tgg	384
Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp	
115 120 125	

aag atg gtt ctt ggg gct cag cgc gaa aac ctc acc acc ggt gca gcg gtt 432
 Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val
 130 135 140
 cta tac cgc tcg gca gat ctt gaa aac tgg gaa ttc tcc ggt gaa atc 480
 Leu Tyr Arg Ser Ala Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu Ile
 145 150 155 160
 acc ttt gac ctc agc gac 498
 Thr Phe Asp Leu Ser Asp
 165

[0078]

<210> 12

<211> 166

<212> PRT

<213> **Corynebacterium thermoaminogenes**

<400> 12

Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly

1 5 10 15

Trp Ala His Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp

20 25 30

Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Val Ser Tyr Asp Leu Asp

35 40 45

Gly Cys Tyr Ser Gly Gly Ala Val Phe Ser Asp Gly Thr Leu Lys Leu

50 55 60

Phe Tyr Thr Gly Asn Arg Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln

65 70 75 80

Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His

85 90 95

Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pr Ala Ser Gly Phe

100

105

110

Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp

115

120

125

Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val

130

135

140

Leu Tyr Arg Ser Ala Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu Ile

145

150

155

160

Thr Phe Asp Leu Ser Asp

165

[0079]

<210> 13

<211> 479

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (1)..(477)

<400> 13

tac tac cag cac gat cca ggt ttc ccc ttc gca cca aag cgc acc ggc 48

Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly

1

5

10

15

tgg gct cac acc acc acg ccg ttg acc gga ccg cag cga ttg cag tgg 96

Trp Ala His Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp

20

25

30

acg cac ctg ccc gac gct ctt tac ccg gat gca tcc tat gac ctg gat 144

Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser Tyr Asp Leu Asp

35

40

45

gga tgc tat tcc ggt gga gcc gta ttt act gac ggc aca ctt aaa ctt 192
 Gly Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly Thr Leu Lys Leu
 50 55 60
 ttc tac acc ggc aac cta aaa att gac ggc aag cgc cgc gcc acc caa 240
 Phe Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln
 65 70 75 80
 aac ctc gtc gaa gtc gag gac cca act ggg ctg atg ggc ggc att cat 288
 Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His
 85 90 95
 cgc cgt tcg cct aaa aat ccg ctt atc gac gga ccc gcc agc ggt ttc 336
 Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe
 100 105 110
 aca ccc cat tac cgc gat ccc atg atc agc cct gat ggt gat ggt tgg 384
 Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp
 115 120 125
 aaa atg gtt ctt ggg gcc caa cgc gaa aac ctc acc ggt gca gcg gtt 432
 Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val
 130 135 140
 cta tac cgc tcg aca gat ctt gaa aac tgg gaa ttc tcc ggt gaa at 479
 Leu Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu
 145 150 155
 【0080】
 <210> 14
 <211> 159
 <212> PRT
 <213> Corynebacterium thermoaminogenes

<400> 14

Tyr Tyr Gln His Asp Pro Gly Phe Pr Phe Ala Pr Lys Arg Thr Gly

1	5	10	15
Trp Ala His Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp			
20	25	30	
Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser Tyr Asp Leu Asp.			
35	40	45	
Gly Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly Thr Leu Lys Leu			
50	55	60	
Phe Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln			
65	70	75	80
Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Ile His			
85	90	95	
Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe			
100	105	110	
Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp			
115	120	125	
Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val			
130	135	140	
Leu Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu			
145	150	155	

【0081】

<210> 15

<211> 490

<212> DNA

<213> Corynebacterium thermoaminogenes

<400> 15

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aatgcattgg ggacacgcac gtagtaaaga tttagttcat tggaaacat taccgattgc 120
tttagaacct ggagatgaag aagaaaaatg ttgtttctc tggtacaggt atagtcaaag 180
atgataagtt gtatTTtattt tatacaggtc accattatta taatgacgat gatcccgatc 240

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attttggca aaatcaaaat atggcttata gtgaagatgg cattcattt caaaaatata 300
aacaaaatgc aatcattcct accccacctg aagataatac acatcaactc agagatccaa 360
aggtaggga acatccatgg ctattattta catgatagta ggttagtcaa atgatagaga 420
attaggacgi attatcttat atcgittctga ggatttataag agggaaattc tggtcctgag 480
atcaatccaa 490

【0082】

<210> 16

<211> 4254

<212> DNA

<213> **Corynebacterium thermoaminogenes**

<220>

<221> CDS

<222> (637)..(1362)

<220>

<221> CDS

<222> (1434)..(2315)

<220>

<221> CDS

<222> (2432)..(3115)

<220>

<221> CDS

<222> (3235)..(4065)

<400> 16

tcacggcgcg cagattaccc agtgtgccgt agagacgctg atcggcattc tcacgcaccc 60
cgcaggtgtt gaagacgatg agatcagggg tgtcaccctc ccccgccgacgt gtgttaaccgg 120

cctcctcgag cagaccggag agacgctcg aatcggtggac gttcatctgg cagccgaagg 180
 tacgcacctc ataggtgcgg gcagtggtgc cttccgggtt cccccgcgcc gggagggtgt 240
 cggcggggtg gtccgggtgg gatggatggg tttcatctg gtgggtatca atctgctg 300
 tcacggagg taattgtatc ggccgcgggc accctgacat aaacgtccga tccagaggaa 360
 cgcaaccccg tggagtgtcg cagccatgca ggttggcaa caccgtaacg gaacctagca 420
 gagtggtagg attgacttca cattcttac ctattgagct attgataaaa tccgggcgga 480
 aatggaaatc acccccacaa atcaccccaa ctgacctgtg gaaagggcga gaaatccagg 540
 gaaattcatt tcaaaatgga ctcaatcaca ggatttaccc cacatgaccc aacattccctt 600
 tatgctatcc ccatgacgca gaccacaaat caccg atg atc aag atg acg ggg 654

Met Ile Lys Met Thr Gly

1 5

gtg cag aag ttc ttc gat gac ttc cag gcc ctg acc gat atc aat ctt 702
 Val Gln Lys Phe Phe Asp Asp Phe Gln Ala Leu Thr Asp Ile Asn Leu

10 15 20

gag gtc ccc gcg gga cag gtc gtt gtt ctc ggc ccg tcc ggt tcc 750
 Glu Val Pro Ala Gly Gln Val Val Val Leu Gly Pro Ser Gly Ser

25 30 35

gga aag tcg acg ctg tgc cgc acc atc aac cgc ctc gaa acc atc gag 798
 Gly Lys Ser Thr Leu Cys Arg Thr Ile Asn Arg Leu Glu Thr Ile Glu

40 45 50

gag gga acc atc gag atc gat gga aaa ctg ctt ccg gag gag ggc aag 846
 Glu Gly Thr Ile Glu Ile Asp Gly Lys Leu Leu Pro Glu Glu Gly Lys

55 60 65 70

gac ctg gcc aag atc cgt gcc gac gtg ggc atg gtg ttc cag tct ttc 894
 Asp Leu Ala Lys Ile Arg Ala Asp Val Gly Met Val Phe Gln Ser Phe

75 80 85

aac ctc ttc ccc cac ctc acc atc aag gac aat gtc acc ctc ggc ccg 942
 Asn Leu Phe Pro His Leu Thr Ile Lys Asp Asn Val Thr Leu Gly Pro

90 95 100

atg aag gtc cgg aag atg aag tcc gag gcc aat gag gtg gcc atg 990
 Met Lys Val Arg Lys Met Lys Lys Ser Glu Ala Asn Glu Val Ala Met
 105 110 115
 aag ctg ttg gaa cgc gtc ggc atc gcc aac cag gcc gag aaa tac ccg 1038
 Lys Leu Leu Glu Arg Val Gly Ile Ala Asn Gln Ala Glu Lys Tyr Pro
 120 125 130
 gca cag ctc tcg ggc ggg cag cag cag cgc gtg gcc atc gcc cgc gca 1086
 Ala Gln Leu Ser Gly Gly Gln Gln Gln Arg Val Ala Ile Ala Arg Ala
 135 140 145 150
 ctg gcg atg aac ccc aag atc atg ctt ttc gac gaa cca acc tcc gcc 1134
 Leu Ala Met Asn Pro Lys Ile Met Leu Phe Asp Glu Pro Thr Ser Ala
 155 160 165
 ctc gac ccc gag atg gtc aac gag gtt ctg gac gtc atg gcg agt ctg 1182
 Leu Asp Pro Glu Met Val Asn Glu Val Leu Asp Val Met Ala Ser Leu
 170 175 180
 gcc aag gaa ggc atg acc atg gtg tgt gtc acc cac gag atg ggt ttc 1230
 Ala Lys Glu Gly Met Thr Met Val Cys Val Thr His Glu Met Gly Phe
 185 190 195
 gca cgc agg gcc gca gac cgt gtg ctg ttc atg tct gac ggc gcc atc 1278
 Ala Arg Arg Ala Ala Asp Arg Val Leu Phe Met Ser Asp Gly Ala Ile
 200 205 210
 gtc gag gac tcc gac ccg gag acc ttc ttc acc aat cca caa acc gac 1326
 Val Glu Asp Ser Asp Pro Glu Thr Phe Phe Thr Asn Pro Gln Thr Asp
 215 220 225 230
 cgg gcg aag gat ttc ctg ggc aag atc ctc gcc cac tgacctcccc 1372
 Arg Ala Lys Asp Phe Leu Gly Lys Ile Leu Ala His
 235 240
 tcactctgtg tccaaactccc ccgcgtggcca aaatcagcga ccatgaccaa caggagcatc 1432
 a atg tcg cac aaa cgc atg ttc acc cgt ctc gcc gca gcc acc agc gca 1481

Met Ser His Lys Arg Met Phe Thr Arg Leu Ala Ala Ala Thr Ser Ala
 245 250 255
 gct gtt ctc gcc ggc atc acc ctc acc gcc tgt ggt gat tcc gag ggt 1529
 Ala Gly Ile Thr Leu Thr Ala Cys Gly Asp Ser Glu Gly
 260 265 270
 ggt gac ggt ctg ctc gcc gcc atc gaa aat ggc aat gtc acc atc ggc 1577
 Gly Asp Gly Leu Leu Ala Ala Ile Glu Asn Gly Asn Val Thr Ile Gly
 275 280 285 290
 acc aag tac gat cag ccg ggt ctg gga ctg cgt aac ccg gac aat tcc 1625
 Thr Lys Tyr Asp Gln Pro Gly Leu Gly Leu Arg Asn Pro Asp Asn Ser
 295 300 305
 atg agc gga ctg gat gtc gac gtc gcg cag tac gtg gtc aac tcc atc 1673
 Met Ser Gly Leu Asp Val Asp Val Ala Gln Tyr Val Val Asn Ser Ile
 310 315 320
 gcc gat gac aac ggt tgg gat cac ccc acc gtg gaa tgg cgc gag acc 1721
 Ala Asp Asp Asn Gly Trp Asp His Pro Thr Val Glu Trp Arg Glu Thr
 325 330 335
 ccc tcc gcc cag cgc gag acc ctc atc cag aac ggt gag gtg gat atg 1769
 Pro Ser Ala Gln Arg Glu Thr Leu Ile Gln Asn Gly Glu Val Asp Met
 340 345 350
 atc gcc gca acc tac tcc atc aac ccc gga cgc tcc gaa tcg gtg aac 1817
 Ile Ala Ala Thr Tyr Ser Ile Asn Pro Gly Arg Ser Glu Ser Val Asn
 355 360 365 370
 ttc ggt gga cca tac ctc ctc acc cac cag gcc ctc ctg gtc cgc gag 1865
 Phe Gly Gly Pro Tyr Leu Leu Thr His Gln Ala Leu Leu Val Arg Glu
 375 380 385
 gac gat gac cgc atc cag acc ctc gag gac ctc gat gac ggc ctg atc 1913
 Asp Asp Asp Arg Ile Gln Thr Leu Glu Asp Leu Asp Asp Gly Leu Ile
 390 395 400

ctg tgt tcc gtt acc gga tcc acc ccc gcc cag aag gtc aag gat gtc 1961
 Leu Cys Ser Val Thr Gly Ser Thr Pro Ala Gln Lys Val Lys Asp Val
 405 410 415
 ctc ccc ggc gtc cag ctg cag gaa tac gac acc tac tcc tcc tgt gtg 2009
 Leu Pro Gly Val Gln Leu Gln Glu Tyr Asp Thr Tyr Ser Ser Cys Val
 420 425 430
 gag gca ctg agc cag ggc aac gtc gat gca atg acc acc gac gcc acc 2057
 Glu Ala Leu Ser Gln Gly Asn Val Asp Ala Met Thr Thr Asp Ala Thr
 435 440 445 450
 atc ctc ttc ggc tac gcg cag cag cgc gaa ggt gaa ttc cgc gtc gtg 2105
 Ile Leu Phe Gly Tyr Ala Gln Gln Arg Glu Gly Glu Phe Arg Val Val
 455 460 465
 gag atg gaa cag gac ggc gag ccg ttc acc aat gag tac tac ggc atc 2153
 Glu Met Glu Gln Asp Gly Glu Pro Phe Thr Asn Glu Tyr Tyr Gly Ile
 470 475 480
 ggt atc acc aag gat gac acc gaa gcc acc gat gcg atc aac gca gcg 2201
 Gly Ile Thr Lys Asp Asp Thr Glu Ala Thr Asp Ala Ile Asn Ala Ala
 485 490 495
 ttg gag cgt atg tac gcc gac ggt tcc ttc cag cgt ttc ctc acc gag 2249
 Leu Glu Arg Met Tyr Ala Asp Gly Ser Phe Gln Arg Phe Leu Thr Glu
 500 505 510
 aac ctc ggc gag gat tcc cag gtt gtc cag gag ggc acc ccg ggt gac 2297
 Asn Leu Gly Glu Asp Ser Gln Val Val Gln Glu Gly Thr Pro Gly Asp
 515 520 525 530
 ctc tcc ttc ctg gac gag tgacctgacg gggccgaacg cccgatgagc 2345
 Leu Ser Phe Leu Asp Glu
 535
 atgcgtggcc cccgcattccc ggggtgccac gcatcatcac tttcaccact gatcccctac 2405
 cgttccttac cgaggagaaa ttcccc atg agt aca tta tgg gcg gat ctg ggt 2458

	Met Ser Thr Leu Trp Ala Asp Leu Gly	
	540	545
ccg tca ctc cta ccc gca ttc tgg gtg aca atc caa ctc acc gtc tat		2506
Pro Ser Leu Leu Pro Ala Phe Trp Val Thr Ile Gln Leu Thr Val Tyr		
550	555	560
tcc gcc atc gga tcc atg atc ctc ggt acc atc ctc acc gcc atg agg		2554
Ser Ala Ile Gly Ser Met Ile Leu Gly Thr Ile Leu Thr Ala Met Arg		
565	570	575
gtg tcc ccg gtg aag atc ctg cgc agc ata tcc acc gcc tac atc aac		2602
Val Ser Pro Val Lys Ile Leu Arg Ser Ile Ser Thr Ala Tyr Ile Asn		
580	585	590
acg gtc cgt aac acc cca ctg acc ctg gtg atc ctg ttc tgt tcc ttc		2650
Thr Val Arg Asn Thr Pro Leu Thr Leu Val Ile Leu Phe Cys Ser Phe		
595	600	605
ggc ctg tat cag aat ctc ggt ctc acc ctc gcc ggt cgc gac agt tcc		2698
Gly Leu Tyr Gln Asn Leu Gly Leu Thr Leu Ala Gly Arg Asp Ser Ser		
610	615	620
acc ttt ctg gcc gat aac aac ttc cgg ctc gcg gtg ctc gga ttc atc		2746
Thr Phe Leu Ala Asp Asn Asn Phe Arg Leu Ala Val Leu Gly Phe Ile		
630	635	640
ctg tac acc tcc gcc ttc gtt gcg gaa tca ctc cgg tca ggc atc aac		2794
Leu Tyr Thr Ser Ala Phe Val Ala Glu Ser Leu Arg Ser Gly Ile Asn		
645	650	655
acc gtg cac ttc ggg cag gcg gag gcc cgg tcg ctg gga ctc ggt		2842
Thr Val His Phe Gly Gln Ala Glu Ala Ala Arg Ser Leu Gly Leu Gly		
660	665	670
ttc agt gac atc ttc cgg tcc atc atc ttc ccc cag gcg gtg cgt gcc		2890
Phe Ser Asp Ile Phe Arg Ser Ile Ile Phe Pro Gln Ala Val Arg Ala		
675	680	685

gcc atc atc ccg ctg ggc aac acc ctc atc gcc ctg acc aag aac acc 2938
 Ala Ile Ile Pro Leu Gly Asn Thr Leu Ile Ala Leu Thr Lys Asn Thr
 690 695 700 705
 acg atc gcg tcc gtg atc ggc gtc ggt gag gcc tcg ctg ctg atg aag 2986
 Thr Ile Ala Ser Val Ile Gly Val Gly Glu Ala Ser Leu Leu Met Lys
 710 715 720
 tcc acg att gaa aat cat gcc aac atg ctc ttc gtc gtg ttc gcc atc 3034
 Ser Thr Ile Glu Asn His Ala Asn Met Leu Phe Val Val Phe Ala Ile
 725 730 735
 ttc gcc gtc ggc ttc atg atc ctc acc ctc ccc atg ggc ctg ggg ctt 3082
 Phe Ala Val Gly Phe Met Ile Leu Thr Leu Pro Met Gly Leu Gly Leu
 740 745 750
 gga aaa ctc gct gag aaa atg gcg gtg aag aaa taatgtcctc ctccgtacgc 3135
 Gly Lys Leu Ala Glu Lys Met Ala Val Lys Lys
 755 760
 gcaacagtcc tctacgacgc ccccggcccc cggggacgca ggtccaacac catcatcacc 3195
 atcgccacca ccctggtggc agtggccgtc ctgttctgg gtg ggc agt gtt ctc 3249
 Val Gly Ser Val Leu
 765
 cag gaa aac ggc cag ttg gac ggc gac aaa tgg acc ccg ttc ctc gat 3297
 Gln Glu Asn Gly Gln Leu Asp Gly Asp Lys Trp Thr Pro Phe Leu Asp
 770 775 780 785
 ccc cag acc tgg acc acc tat ctt ctg ccc ggc ctg tgg gga acc ctg 3345
 Pro Gln Thr Trp Thr Tyr Leu Leu Pro Gly Leu Trp Gly Thr Leu
 790 795 800
 aag gca gcg gtg gcc tcc atc ctt ctc gcg ctg atg ggc acc ctg 3393
 Lys Ala Ala Val Ala Ser Ile Leu Leu Ala Leu Ile Met Gly Thr Leu
 805 810 815
 ctc ggg ctc gga cgc atc tcc gaa atc cgg ctc ctg cgc tgg ttc tgc 3441

Leu Gly Leu Gly Arg Ile Ser Glu Ile Arg Leu L u Arg Trp Phe Cys
 820 825 830
 ggg atc atc atc gag acc ttc cgt gcc atc ccg gtg ctg atc ctc atg 3489
 Gly Ile Ile Ile Glu Thr Phe Arg Ala Ile Pro Val Leu Ile Leu Met
 835 840 845
 atc ttc gcc tat cag ttg ttc gcc cgt tac cag ctc gtt cca tca cgc 3537
 Ile Phe Ala Tyr Gln Leu Phe Ala Arg Tyr Gln Leu Val Pro Ser Arg
 850 855 860 865
 cag ctg gcc ttc gcc gcg gtg gtc ttc ggt ctc acc atg tac aac ggc 3585
 Gln Leu Ala Phe Ala Ala Val Val Phe Gly Leu Thr Met Tyr Asn Gly
 870 875 880
 tcc gtc atc gcc gag atc ctt aga tcg ggt atc gcc tcc ctg ccg aag 3633
 Ser Val Ile Ala Glu Ile Leu Arg Ser Gly Ile Ala Ser Leu Pro Lys
 885 890 895
 gga cag cgt gag gcg gcg atc gcc ctg ggc atg tca acc cgc cag acc 3681
 Gly Gln Arg Glu Ala Ala Ile Ala Leu Gly Met Ser Thr Arg Gln Thr
 900 905 910
 acc tgg tcg atc ctg ctc ccc cag gcg gtg gca gcg atg ctg ccc gcc 3729
 Thr Trp Ser Ile Leu Leu Pro Gln Ala Val Ala Ala Met Leu Pro Ala
 915 920 925
 ctg atc gcg cag atg gtc atc gcg ctg aag gac tcc gcc ctc ggt tac 3777
 Leu Ile Ala Gln Met Val Ile Ala Leu Lys Asp Ser Ala Leu Gly Tyr
 930 935 940 945
 cag atc ggt tat atc gag gtg gta cgc tcc ggt atc cag tcc gca tcc 3825
 Gln Ile Gly Tyr Ile Glu Val Val Arg Ser Gly Ile Gln Ser Ala Ser
 950 955 960
 gtc aac cgg aac tac ctg gct gcc ctc gcg gtg gtc gcg gtc atc atg 3873
 Val Asn Arg Asn Tyr Leu Ala Ala Leu Ala Val Val Ala Val Ile Met
 965 970 975

atc ctg atc aac ttc gca ctg acc gca ctg gca gag cgt atc cag cgt 3921
 Ile Leu Ile Asn Phe Ala Leu Thr Ala Leu Ala Glu Arg Ile Gln Arg
 980 985 990
 cag ctg cgt gcc gga cgt gcc cgc agg aac att gtg gca aag gtg ccc 3969
 Gln Leu Arg Ala Gly Arg Ala Arg Arg Asn Ile Val Ala Lys Val Pro
 995 1000 1005
 gag gaa ccc gat cag ggc ctg gat acc aag gac aat gtg aac gtg gat 4017
 Glu Glu Pro Asp Gln Gly Leu Asp Thr Lys Asp Asn Val Asn Val Asp
 1010 1015 1020 1025
 tgg cac gat ccc gat tac aag gaa gtc aaa cac ccg gga ccg tca ttc 4065
 Trp His Asp Pro Asp Tyr Lys Glu Val Lys His Pro Gly Pro Ser Phe
 1030 1035 1040
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 cccagatgtc tggggcagcc ggactttgtg gcagatcaat gctgactgag gtcctcgatg 4185
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 gcaagtgct 4254

【0083】

<210> 17

<211> 242

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 17

Met Ile Lys Met Thr Gly Val Gln Lys Phe Phe Asp Asp Phe Gln Ala

1 5 10 15

Leu Thr Asp Ile Asn Leu Glu Val Pro Ala Gly Gln Val Val Val Val

20 25 30

Leu Gly Pr Ser Gly Ser Gly Lys Ser Thr Leu Cys Arg Thr Ile Asn

35 40 45

Arg Leu Glu Thr Ile Glu Glu Gly Thr Ile Glu Ile Asp Gly Lys Leu
 50 55 60
 Leu Pro Glu Glu Gly Lys Asp Leu Ala Lys Ile Arg Ala Asp Val Gly
 65 70 75 80
 Met Val Phe Gln Ser Phe Asn Leu Phe Pro His Leu Thr Ile Lys Asp
 85 90 95
 Asn Val Thr Leu Gly Pro Met Lys Val Arg Lys Met Lys Lys Ser Glu
 100 105 110
 Ala Asn Glu Val Ala Met Lys Leu Leu Glu Arg Val Gly Ile Ala Asn
 115 120 125
 Gln Ala Glu Lys Tyr Pro Ala Gln Leu Ser Gly Gly Gln Gln Gln Arg
 130 135 140
 Val Ala Ile Ala Arg Ala Leu Ala Met Asn Pro Lys Ile Met Leu Phe
 145 150 155 160
 Asp Glu Pro Thr Ser Ala Leu Asp Pro Glu Met Val Asn Glu Val Leu
 165 170 175
 Asp Val Met Ala Ser Leu Ala Lys Glu Gly Met Thr Met Val Cys Val
 180 185 190
 Thr His Glu Met Gly Phe Ala Arg Arg Ala Ala Asp Arg Val Leu Phe
 195 200 205
 Met Ser Asp Gly Ala Ile Val Glu Asp Ser Asp Pro Glu Thr Phe Phe
 210 215 220
 Thr Asn Pro Gln Thr Asp Arg Ala Lys Asp Phe Leu Gly Lys Ile Leu
 225 230 235 240
 Ala His

【0084】

<210> 18

<211> 294

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 18

Met Ser His Lys Arg Met Phe Thr Arg Leu Ala Ala Ala Thr Ser Ala
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 20 25 30
 Gly Asp Gly Leu Leu Ala Ala Ile Glu Asn Gly Asn Val Thr Ile Gly
 35 40 45
 Thr Lys Tyr Asp Gln Pro Gly Leu Gly Leu Arg Asn Pro Asp Asn Ser
 50 55 60
 Met Ser Gly Leu Asp Val Asp Val Ala Gln Tyr Val Val Asn Ser Ile
 65 70 75 80
 Ala Asp Asp Asn Gly Trp Asp His Pro Thr Val Glu Trp Arg Glu Thr
 85 90 95
 Pro Ser Ala Gln Arg Glu Thr Leu Ile Gln Asn Gly Glu Val Asp Met
 100 105 110
 Ile Ala Ala Thr Tyr Ser Ile Asn Pro Gly Arg Ser Glu Ser Val Asn
 115 120 125
 Phe Gly Gly Pro Tyr Leu Leu Thr His Gln Ala Leu Leu Val Arg Glu
 130 135 140
 Asp Asp Asp Arg Ile Gln Thr Leu Glu Asp Leu Asp Asp Gly Leu Ile
 145 150 155 160
 Leu Cys Ser Val Thr Gly Ser Thr Pro Ala Gln Lys Val Lys Asp Val
 165 170 175
 Leu Pro Gly Val Gln Leu Gln Glu Tyr Asp Thr Tyr Ser Ser Cys Val
 180 185 190
 Glu Ala L u Ser Gln Gly Asn Val Asp Ala Met Thr Thr Asp Ala Thr
 195 200 205

Ile Leu Phe Gly Tyr Ala Gln Gln Arg Glu Gly Glu Phe Arg Val Val

210 215 220

Glu Met Glu Gln Asp Gly Glu Pro Phe Thr Asn Glu Tyr Tyr Gly Ile

225 230 235 240

Gly Ile Thr Lys Asp Asp Thr Glu Ala Thr Asp Ala Ile Asn Ala Ala

245 250 255

Leu Glu Arg Met Tyr Ala Asp Gly Ser Phe Gln Arg Phe Leu Thr Glu

260 265 270

Asn Leu Gly Glu Asp Ser Gln Val Val Gln Glu Gly Thr Pro Gly Asp

275 280 285

Leu Ser Phe Leu Asp Glu

290

[0085]

<210> 19

<211> 228

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 19

Met Ser Thr Leu Trp Ala Asp Leu Gly Pro Ser Leu Leu Pro Ala Phe

1 5 10 15

Trp Val Thr Ile Gln Leu Thr Val Tyr Ser Ala Ile Gly Ser Met Ile

20 25 30

Leu Gly Thr Ile Leu Thr Ala Met Arg Val Ser Pro Val Lys Ile Leu

35 40 45

Arg Ser Ile Ser Thr Ala Tyr Ile Asn Thr Val Arg Asn Thr Pro Leu

50 55 60

Thr Leu Val Ile Leu Phe Cys Ser Phe Gly Leu Tyr Gln Asn L u Gly

65 70 75 80

Leu Thr Leu Ala Gly Arg Asp Ser Ser Thr Phe Leu Ala Asp Asn Asn

85 90 95

Phe Arg Leu Ala Val Leu Gly Phe Ile Leu Tyr Thr Ser Ala Phe Val

100 105 110

Ala Glu Ser Leu Arg Ser Gly Ile Asn Thr Val His Phe Gly Gln Ala

115 120 125

Glu Ala Ala Arg Ser Leu Gly Leu Gly Phe Ser Asp Ile Phe Arg Ser

130 135 140

Ile Ile Phe Pro Gln Ala Val Arg Ala Ala Ile Ile Pro Leu Gly Asn

145 150 155 160

Thr Leu Ile Ala Leu Thr Lys Asn Thr Thr Ile Ala Ser Val Ile Gly

165 170 175

Val Gly Glu Ala Ser Leu Leu Met Lys Ser Thr Ile Glu Asn His Ala

180 185 190

Asn Met Leu Phe Val Val Phe Ala Ile Phe Ala Val Gly Phe Met Ile

195 200 205

Leu Thr Leu Pro Met Gly Leu Gly Lys Leu Ala Glu Lys Met

210 215 220

Ala Val Lys Lys

225

【0086】

<210> 20

<211> 277

<212> PRT

<213> *Corynebacterium thermoaminogenes*

<400> 20

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1 5 10 15

Thr Pro Ph Leu Asp Pro Gln Thr Trp Thr Thr Tyr Leu Leu Pro Gly
 20 25 30
 Leu Trp Gly Thr Leu Lys Ala Ala Val Ala Ser Ile Leu Leu Ala Leu
 35 40 45
 Ile Met Gly Thr Leu Leu Gly Leu Gly Arg Ile Ser Glu Ile Arg Leu
 50 55 60
 Leu Arg Trp Phe Cys Gly Ile Ile Ile Glu Thr Phe Arg Ala Ile Pro
 65 70 75 80
 Val Leu Ile Leu Met Ile Phe Ala Tyr Gln Leu Phe Ala Arg Tyr Gln
 85 90 95
 Leu Val Pro Ser Arg Gln Leu Ala Phe Ala Ala Val Val Phe Gly Leu
 100 105 110
 Thr Met Tyr Asn Gly Ser Val Ile Ala Glu Ile Leu Arg Ser Gly Ile
 115 120 125
 Ala Ser Leu Pro Lys Gly Gln Arg Glu Ala Ala Ile Ala Leu Gly Met
 130 135 140
 Ser Thr Arg Gln Thr Thr Trp Ser Ile Leu Leu Pro Gln Ala Val Ala
 145 150 155 160
 Ala Met Leu Pro Ala Leu Ile Ala Gln Met Val Ile Ala Leu Lys Asp
 165 170 175
 Ser Ala Leu Gly Tyr Gln Ile Gly Tyr Ile Glu Val Val Arg Ser Gly
 180 185 190
 Ile Gln Ser Ala Ser Val Asn Arg Asn Tyr Leu Ala Ala Leu Ala Val
 195 200 205
 Val Ala Val Ile Met Ile Leu Ile Asn Phe Ala Leu Thr Ala Leu Ala
 210 215 220
 Glu Arg Ile Gln Arg Gln Leu Arg Ala Gly Arg Ala Arg Arg Asn Ile
 225 230 235 240
 Val Ala Lys Val Pro Glu Glu Pro Asp Gln Gly Leu Asp Thr Lys Asp

245 250 255
 Asn Val Asn Val Asp Trp His Asp Pro Asp Tyr Lys Glu Val Lys His
 260 265 270
 Pro Gly Pro Ser Phe
 275

[0087]

<210> 21

<211> 3598

<212> DNA

<213> *Corynebacterium thermoaminogenes*

<220>

<221> CDS

<222> (454)..(3222)

<400> 21

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 aaccgcgggt gacacccctg ccatttgggc agctcccccc acctcaccat gtccacattt 120
 tccataatgt ggccctgtAAC acccttggc tcaaggcttc cacgccccac cgggaccctc 180
 atcagcagggt gaaacagacc ctccgtcaat gctttgttaa aaagaaccgc ctttgtgcg 240
 tatccttgtg tcaattgtgc ggcactgcc accagcttc ctcaggattt aacacggtcg 300
 ggaaatcctc cccggatacc ctgcacgccc cacctccac accgacaccg gcggggaggg 360
 ccgggcacgt tttagctgc gggtagatgga agcggtcgcc ggtccccgg tcgcataaac 420
 gaaatgaaaa acattccaac aggagggttg gaa atg gcc gat caa gca aaa ctt 474

Met Ala Asp Gln Ala Lys Leu

1	5	
ggt ggc aaa ccc aca gat gac acc aac ttc gcg atg atc cgt gat ggc	522	
Gly Gly Lys Pr Thr Asp Asp Thr Asn Phe Ala Met Ile Arg Asp Gly		

10	15	20
gtt gca tct tat ttg aac gac tcc gac ccg gag gag acc aag gag tgg	570	
Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Lys Glu Trp		

25	30	35	
atg gac tcc cta gac ggt cta ctg cag gat tcc tct ccg gag cgc gcc 618			
Met Asp Ser Leu Asp Gly Leu Leu Gln Asp Ser Ser Pro Glu Arg Ala			
40	45	50	55
cgt tac ctg atg ctg cgc ctg ctg gag cgg gca tcc gcc aag cgt gtc 666			
Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys Arg Val			
60	65	70	
cca ctg ccc ccg atg acg tcc acc gat tac gtc aac acc atc ccc aca 714			
Pro Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile Pro Thr			
75	80	85	
tcc atg gag ccc gat ttc ccg ggt gat gag gag atg gag aag cgc tac 762			
Ser Met Glu Pro Asp Phe Pro Gly Asp Glu Glu Met Glu Lys Arg Tyr			
90	95	100	
cgc cgc tgg atg cgc tgg aac gcc gcc atc atg gtg cac cgt gcc cag 810			
Arg Arg Trp Met Arg Trp Asn Ala Ala Ile Met Val His Arg Ala Gln			
105	110	115	
cgc ccg gga atc ggt gtg ggt ggg cac atc tcc acc tac gcc ggc gcc 858			
Arg Pro Gly Ile Gly Val Gly Gly His Ile Ser Thr Tyr Ala Gly Ala			
120	125	130	135
gcc cca ctc tac gag gtc ggt ttc aac cac ttc ttc cgc ggc aag gac 906			
Ala Pro Leu Tyr Glu Val Gly Phe Asn His Phe Phe Arg Gly Lys Asp			
140	145	150	
cac ccg ggt ggc ggt gac cag gtc ttc ttc cag ggt cac gcc tcc ccg 954			
His Pro Gly Gly Asp Gln Val Phe Phe Gln Gly His Ala Ser Pro			
155	160	165	
ggc atg tac gcc cgc gcc ttc ctc gag ggc cgt ctc acc gag agc gat 1002			
Gly Met Tyr Ala Arg Ala Phe Leu Glu Gly Arg Leu Thr Glu Ser Asp			
170	175	180	
ctg gac agc ttc cgc cag gag gtc tcc tac gaa ggt ggt ggc atc ccg 1050			

Leu Asp Ser Phe Arg Gln Glu Val Ser Tyr Glu Gly Gly Gly Ile Pro
 185 190 195
 tcc tac ccg cac ccg cac ggc atg ccg gac ttc tgg gag ttc ccg acc 1098
 Ser Tyr Pro His Pro His Gly Met Pro Asp Phe Trp Glu Phe Pro Thr
 200 205 210 215
gtg tcc atg ggc ctc ggg ccc atg gat gcc atc tac cag gcg cgc ttc 1146
 Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg Phe
 220 225 230
 aac cgc tac ctc cac aac cgt ggc atc aag gac acc tcg gag cag cac 1194
 Asn Arg Tyr Leu His Asn Arg Gly Ile Lys Asp Thr Ser Glu Gln His
 235 240 245
 gtc tgg gca ttc ctc ggt gac ggc gag atg gat gag ccg gag tcc cgt 1242
 Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser Arg
 250 255 260
 ggt ctc atc cac cag gct gcg ctg aac aac ctg gac aac ctc acc ttc 1290
 Gly Leu Ile His Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr Phe
 265 270 275
 gtg atc aac tgc aac ctg cag cgt ctt gat ggc ccg gtc cgc ggt aac 1338
 Val Ile Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly Asn
 280 285 290 295
 acc aag atc atc cag gaa ctc gag tcc ttc ttc cgt ggt gcc ggc tgg 1386
 Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly Trp
 300 305 310
 tcc gtc atc aag gtc atc tgg ggc cgt gag tgg gat gaa ctg ctg gag 1434
Ser Val Ile Lys Val Ile Trp Gly Arg Glu Trp Asp Glu Leu Leu Glu
 315 320 325
 aag gac cag gac ggt gct ctt gtc gag gtc atg aac aac acc tcc gac 1482
 Lys Asp Gln Asp Gly Ala Leu Val Glu Val Met Asn Asn Thr Ser Asp
 330 335 340

ggt gac tac cag acc ttc aag gcc aat gac ggt gcc tac gtc cgt gag 1530
 Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg Glu
 345 350 355
 cac ttc ttc ggc cgt gac ccc cgc acc ctc aag ctc gtc gag gac atg 1578
 His Phe Phe Gly Arg Asp Pro Arg Thr Leu Lys Leu Val Glu Asp Met
 360 365 370 375
 acc gac gag gag atc tgg aag ctg ccc cgt ggt ggc cat gac tac cgt 1626
 Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr Arg
 380 385 390
 aag gtc tac gcc gcc tac aag cgt gcg ctg gag acc aag gac cgc ccg 1674
 Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg Pro
 395 400 405
 acc gtc att ctc gcc cat acc atc aag ggc tac ggc ctg ggc cac aac 1722
 Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His Asn
 410 415 420
 ttc gag ggc cgc aac gcg acc cac cag atg aag aag ctg acc ctg gat 1770
 Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu Asp
 425 430 435
 gac ctg aag ctg ttc cgt gac aag cag ggt ctg ccc atc acc gat gag 1818
 Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Leu Pro Ile Thr Asp Glu
 440 445 450 455
 gag ctg gag aag gat ccc tac ctg cct ccg tac tac cac ccg ggt gag 1866
 Glu Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly Glu
 460 465 470
 gac gca ccg gag atc aag tac atg aag gag cgt cgc cag gcg ctc ggt 1914
 Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Gln Ala Leu Gly
 475 480 485
 ggt ttc ctg ccg gag cgc cgt gag aag tac gag cca ctg cag gtt ccc 1962
 Gly Phe Leu Pro Glu Arg Arg Glu Lys Tyr Glu Pro Leu Gln Val Pro

490	495	500	
ccg ctg gac aag ctg cgg tcc gtg cgc aag ggt tcc ggc aag cag cag			2010
Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln Gln			
505	510	515	
gtg gcc acc acc atg gcc acg gtg cgt acc ttc aag gaa ctc atg cgg			2058
Val Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met Arg			
520	525	530	535
gac aag aac ctg gcc gac cgc ttg gtc ccg atc atc ccg gat gag gcc			2106
Asp Lys Asn Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu Ala			
540	545	550	
cgc acc ttc ggc ctg gac tcc tgg ttc ccg acc ctg aaa atc tac aac			2154
Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr Asn			
555	560	565	
ccg cac ggt cag aac tac gtg ccg gtc gac cat gac ctc atg ctg tcc			2202
Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu Ser			
570	575	580	
tac cgt gag gcc aag gac ggc cag atc ctg cat gag ggc atc aac gag			2250
Tyr Arg Glu Ala Lys Asp Gly Gln Ile Leu His Glu Gly Ile Asn Glu			
585	590	595	
gcc ggt tcc gtg gca tcg ttt atc gcc ggc gga acc tcc tac gcc acc			2298
Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr Ser Tyr Ala Thr			
600	605	610	615
cat ggc gag gcc atg atc ccg ctg tac atc ttc tac tcg atg ttc ggc			2346
His Gly Glu Ala Met Ile Pro Leu Tyr Ile Phe Tyr Ser Met Phe Gly			
620	625	630	
ttc cag cgc acc ggt gac ggc atc tgg gcc gca gcc gac cag atg acg			2394
Phe Gln Arg Thr Gly Asp Gly Ile Trp Ala Ala Asp Gln Met Thr			
635	640	645	
cgt ggt ttc ctc ctg ggc gcc acc gcc ggt cgc acc acc ctg acc ggt			2442

Arg Gly Phe Leu Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly
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 gag ggc ctc cag cac atg gat ggc cac tcc ccg atc ctg gcc tcc acc 2490
 Glu Gly Leu Gln His Met Asp Gly His Ser Pro Ile Leu Ala Ser Thr
 665 670 675
 aac ccc ggt gtg gag acc tat gac ccg gcg ttc tcc tac gag atc gcg 2538
 Asn Pro Gly Val Glu Thr Tyr Asp Pro Ala Phe Ser Tyr Glu Ile Ala
 680 685 690 695
 cac ctc gtc cac cgc ggc atc gac cgc atg tac gga ccg ggc aag ggt 2586
 His Leu Val His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly Lys Gly
 700 705 710
 gag aat gtc atc tac tac ctc acc atc tac aac gag cca acc ccg cag 2634
 Glu Asn Val Ile Tyr Tyr Leu Thr Ile Tyr Asn Glu Pro Thr Pro Gln
 715 720 725
 ccg gct gag cct gag gat ctg gac gtc gag ggc ctg cac aag ggc atc 2682
 Pro Ala Glu Pro Glu Asp Leu Asp Val Glu Gly Leu His Lys Gly Ile
 730 735 740
 tac ctc tac gac aag gcc gcc gag ggt gag ggc cat gag gcc tcg atc 2730
 Tyr Leu Tyr Asp Lys Ala Ala Glu Gly Glu Gly His Glu Ala Ser Ile
 745 750 755
 ctg gcc tcc ggc atc ggc atg cag tgg gca ctg cgc gcc cgt gac atc 2778
 Leu Ala Ser Gly Ile Gly Met Gln Trp Ala Leu Arg Ala Arg Asp Ile
 760 765 770 775
 ctc gcc gag gat tac ggc atc cgt gcc aac atc ttc tcc gcc acc tcg 2826
 Leu Ala Glu Asp Tyr Gly Ile Arg Ala Asn Ile Phe Ser Ala Thr Ser
 780 785 790
 tgg gtg gag ctg gcc cgc gac ggt gcc cgc cgt aac ctg gag ggc ctg 2874
 Trp Val Glu Leu Ala Arg Asp Gly Ala Arg Arg Asn Leu Glu Ala Leu
 795 800 805

cgc aac ccg ggt gcg gat gtc ggt gag gca ttc gtg acc acc cag ctg 2922
 Arg Asn Pro Gly Ala Asp Val Gly Glu Ala Phe Val Thr Thr Gln Leu
 810 815 820
 aag aag ggt tcc ggc ccc tac gtc gcg gtg tcc gac ttc gcg acc gac 2970
 Lys Lys Gly Ser Gly Pro Tyr Val Ala Val Ser Asp Phe Ala Thr Asp
 825 830 835
 ctg ccg aac cag atc cgc gag tgg gtt ccc ggt gac tac atc gtc ctc 3018
 Leu Pro Asn Gln Ile Arg Glu Trp Val Pro Gly Asp Tyr Ile Val Leu
 840 845 850 855
 ggt gcc gac ggc ttc ggt ttc tcc gat acc cgt ccg gca gcc cgt cgt 3066
 Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg
 860 865 870
 tac ttc aac atc gac gcc gag tcc atc gtc gtg gcg gtc ctg cgc ggc 3114
 Tyr Phe Asn Ile Asp Ala Glu Ser Ile Val Val Ala Val Leu Arg Gly
 875 880 885
 ctg gtc cgc gag ggt gtc atc gat gcc tcc gtg gcg gcg cac gcg gct 3162
 Leu Val Arg Glu Gly Val Ile Asp Ala Ser Val Ala Ala His Ala Ala
 890 895 900
 gag aag tac aag ctg tcc gac ccg acg gca cca cag gtc gat ccg gac 3210
 Glu Lys Tyr Lys Leu Ser Asp Pro Thr Ala Pro Gln Val Asp Pro Asp
 905 910 915
 gca ccg atc gag tagacctgct tgtcgacgaa aaacacccccc gccccctcac 3262
 Ala Pro Ile Glu
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 acggtgagct tctgcttcac ctctgcgcgt gcctcataga cgatccgtcc ctcgtgcac 3442
 atgatgagggc ggttacccag gcggatagcc tggatgtgt tggtgggtgac catgagggtg 3502
 gtcagtttgc cgtccctcgac gatcttctcg gtcagggtgg tgaccagttc ggctcgctgg 3562

gggtccaggg cggcggtgtc ttcgtcgaga agcatg 3598

[0088]

<210> 22

<211> 923

<212> PRT

<213> *Corynebacterium thermoaminogenes*

<400> 22

Met Ala Asp Gln Ala Lys Leu Gly Gly Lys Pro Thr Asp Asp Thr Asn

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Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp

20 25 30

Pro Glu Glu Thr Lys Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln

35 40 45

Asp Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu

50 55 60

Arg Ala Ser Ala Lys Arg Val Pro Leu Pro Pro Met Thr Ser Thr Asp

65 70 75 80

Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Asp Phe Pro Gly Asp

85 90 95

Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Met Arg Trp Asn Ala Ala

100 105 110

Ile Met Val His Arg Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His

115 120 125

Ile Ser Thr Tyr Ala Gly Ala Ala Pro Leu Tyr Glu Val Gly Phe Asn

130 135 140

His Phe Phe Arg Gly Lys Asp His Pro Gly Gly Asp Gln Val Phe

145 150 155 160

Phe Gln Gly His Ala Ser Pr Gly Met Tyr Ala Arg Ala Phe Leu Glu

165	170	175
Gly Arg Leu Thr Glu Ser Asp Leu Asp Ser Phe Arg	Gln Glu Val Ser	
180	185	190
Tyr Glu Gly Gly Ile Pro Ser Tyr Pro His Pro His	Gly Met Pro	
195	200	205
Asp Phe Trp-Glu-Phe Pro Thr-Val-Ser-Met-Gly-Leu-Gly-Pro-Met Asp		
210	215	220
Ala Ile Tyr Gln Ala Arg Phe Asn Arg Tyr Leu His Asn Arg Gly Ile		
225	230	235
Lys Asp Thr Ser Glu Gln His Val Trp Ala Phe Leu Gly Asp Gly Glu		
245	250	255
Met Asp Glu Pro Glu Ser Arg Gly Leu Ile His Gln Ala Ala Leu Asn		
260	265	270
Asn Leu Asp Asn Leu Thr Phe Val Ile Asn Cys Asn Leu Gln Arg Leu		
275	280	285
Asp Gly Pro Val Arg Gly Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser		
290	295	300
Phe Phe Arg Gly Ala Gly Trp Ser Val Ile Lys Val Ile Trp Gly Arg		
305	310	315
Glu Trp Asp Glu Leu Leu Glu Lys Asp Gln Asp Gly Ala Leu Val Glu		
325	330	335
Val Met Asn Asn Thr Ser Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn		
340	345	350
Asp Gly Ala Tyr Val Arg Glu His Phe Phe Gly Arg Asp Pro Arg Thr		
355	360	365
Leu Lys Leu Val Glu Asp Met Thr Asp Glu Glu Ile Trp Lys Leu Pr		
370	375	380
Arg Gly Gly His Asp Tyr Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala		
385	390	395
		400

Leu Glu Thr Lys Asp Arg Pro Thr Val Ile Leu Ala His Thr Ile Lys
 405 410 415
 Gly Tyr Gly Leu Gly His Asn Phe Glu Gly Arg Asn Ala Thr His Gln
 420 425 430
 Met Lys Lys Leu Thr Leu Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln
 435 440 445
 Gly Leu Pro Ile Thr Asp Glu Glu Leu Glu Lys Asp Pro Tyr Leu Pro
 450 455 460
 Pro Tyr Tyr His Pro Gly Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys
 465 470 475 480
 Glu Arg Arg Gln Ala Leu Gly Gly Phe Leu Pro Glu Arg Arg Glu Lys
 485 490 495
 Tyr Glu Pro Leu Gln Val Pro Pro Leu Asp Lys Leu Arg Ser Val Arg
 500 505 510
 Lys Gly Ser Gly Lys Gln Gln Val Ala Thr Thr Met Ala Thr Val Arg
 515 520 525
 Thr Phe Lys Glu Leu Met Arg Asp Lys Asn Leu Ala Asp Arg Leu Val
 530 535 540
 Pro Ile Ile Pro Asp Glu Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe
 545 550 555 560
 Pro Thr Leu Lys Ile Tyr Asn Pro His Gly Gln Asn Tyr Val Pro Val
 565 570 575
 Asp His Asp Leu Met Leu Ser Tyr Arg Glu Ala Lys Asp Gly Gln Ile
 580 585 590
 Leu His Glu Gly Ile Asn Glu Ala Gly Ser Val Ala Ser Phe Ile Ala
 595 600 605
 Ala Gly Thr Ser Tyr Ala Thr His Gly Glu Ala Met Ile Pr Leu Tyr
 610 615 620
 Ile Phe Tyr Ser Met Phe Gly Phe Gln Arg Thr Gly Asp Gly Ile Trp

625	630	635	640
Ala Ala Ala Asp Gln Met Thr Arg Gly Phe Leu Leu Gly Ala Thr Ala			
645	650	655	
Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln His Met Asp Gly His			
660	665	670	
Ser Pro Ile Leu Ala Ser Thr Asn Pro Gly Val Glu Thr Tyr Asp Pro			
675	680	685	
Ala Phe Ser Tyr Glu Ile Ala His Leu Val His Arg Gly Ile Asp Arg			
690	695	700	
Met Tyr Gly Pro Gly Lys Gly Glu Asn Val Ile Tyr Tyr Leu Thr Ile			
705	710	715	720
Tyr Asn Glu Pro Thr Pro Gln Pro Ala Glu Pro Glu Asp Leu Asp Val			
725	730	735	
Glu Gly Leu His Lys Gly Ile Tyr Leu Tyr Asp Lys Ala Ala Glu Gly			
740	745	750	
Glu Gly His Glu Ala Ser Ile Leu Ala Ser Gly Ile Gly Met Gln Trp			
755	760	765	
Ala Leu Arg Ala Arg Asp Ile Leu Ala Glu Asp Tyr Gly Ile Arg Ala			
770	775	780	
Asn Ile Phe Ser Ala Thr Ser Trp Val Glu Leu Ala Arg Asp Gly Ala			
785	790	795	800
Arg Arg Asn Leu Glu Ala Leu Arg Asn Pro Gly Ala Asp Val Gly Glu			
805	810	815	
Ala Phe Val Thr Thr Gln Leu Lys Gly Ser Gly Pro Tyr Val Ala			
820	825	830	
Val Ser Asp Phe Ala Thr Asp Leu Pr Asn Gln Ile Arg Glu Trp Val			
835	840	845	
Pr Gly Asp Tyr Ile Val Leu Gly Ala Asp Gly Phe Gly Phe Ser Asp			
850	855	860	

Thr Arg Pro Ala Ala Arg Arg Tyr Phe Asn Ile Asp Ala Glu Ser Ile
 865 870 875 880

Val Val Ala Val Leu Arg Gly Leu Val Arg Glu Gly Val Ile Asp Ala
 885 890 895

Ser Val Ala Ala His Ala Ala Glu Lys Tyr Lys Leu Ser Asp Pro Thr
 900 905 910

Ala Pro Gln Val Asp Pro Asp Ala Pro Ile Glu
 915 920

<210> 23

<211> 4013

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (319)..(3735)

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 cggcaatggg ggtctcgggc gggggcatt ctttcacgg caaggtggc aaattccgca 180
 ggtcaactccc cggccggcgg tagagaacgg agcgaaaacg gaaagcaata cgtggtttc 240
 cggactggcc gttacgatgt tctgaagagt gactgccatc acccaacagg ctggccctcg 300
 tcgaaaggaa caaaaact gtg gtt aca aca aca ccc tcc acg ctg ccg gcg 351

Val Val Thr Thr Pro Ser Thr Leu Pro Ala

1 5 10

ttc aaa aag atc ctg gtg gcc aac cga ggt gaa atc gcg gtg cga gca 399
 Phe Lys Lys Ile Leu Val Ala Asn Arg Gly Glu Ile Ala Val Arg Ala

15	20	25	
ttc cgc gcc gcc tac gag acc ggg gcc gca acc gtg gcc atc tac ccc			447
Phe Arg Ala Ala Tyr Glu Thr Gly Ala Ala Thr Val Ala Ile Tyr Pro			
30	35	40	
cgg gag gac cgt ggc tcc ttc cac cgc tcc ttc gcc tcc gag gcg gtg			495
Arg Glu Asp Arg Gly Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val			
45	50	55	
agg atc gga acc gag ggc tca ccc gtc aag gcg tac ctc gat att gat			543
Arg Ile Gly Thr Glu Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp			
60	65	70	75
gag atc atc aac gcc gcc aag aag gtg aaa gcg gac gcg gtc tac ccg			591
Glu Ile Ile Asn Ala Ala Lys Lys Val Lys Ala Asp Ala Val Tyr Pro			
80	85	90	
ggg tat ggt ttc ctt tcg gaa aat gcc cag ctc gcg cgt gaa tgc gcg			639
Gly Tyr Gly Phe Leu Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala			
95	100	105	
gag aac ggc att acc ttc atc ggt ccc acc ccg gag gtg ctc gac ctc			687
Glu Asn Gly Ile Thr Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu			
110	115	120	
acg ggc gac aag tcc aag gct gtg tcc gcc gcg aag aag gcc ggg ctg			735
Thr Gly Asp Lys Ser Lys Ala Val Ser Ala Ala Lys Lys Ala Gly Leu			
125	130	135	
ccg gtg ctg gcg gaa tcc acc ccc agc acc gac atc gat gag atc gtc			783
Pro Val Leu Ala Glu Ser Thr Pro Ser Thr Asp Ile Asp Glu Ile Val			
140	145	150	155
aag agt gcc gag ggg cag acc tac ccg atc ttc gtc aag gcc gtc gca			831
Lys Ser Ala Glu Gly Gln Thr Tyr Pr Ile Phe Val Lys Ala Val Ala			
160	165	170	
ggt ggt ggc ggg cgt ggt atg cgg ttc gtc gag aag ccc gag gac ctg			879

Gly Gly Gly Gly Arg Gly Met Arg Phe Val Glu Lys Pro Glu Asp Leu
 175 180 185
 cgt gag ctg gcc agg gag gcc tcc cgc gag gcg gag gcc gct ttc ggt 927
 Arg Glu Leu Ala Arg Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly
 190 195 200
 gac gga tcc gtc tac gtc gaa cgg gcc gtg atc aaa ccc cag cac atc 975
 Asp Gly Ser Val Tyr Val Glu Arg Ala Val Ile Lys Pro Gln His Ile
 .. 205 210 215
 gag gtg cag atc ctc ggt gat cac acc ggc gat gtc atc cac ctg tat 1023
 Glu Val Gln Ile Leu Gly Asp His Thr Gly Asp Val Ile His Leu Tyr
 220 225 230 235
 gaa cgc gac tgt tcc ctg cag cgc cgc cac cag aag gtc gtg gag atc 1071
 Glu Arg Asp Cys Ser Leu Gln Arg Arg His Gln Lys Val Val Glu Ile
 240 245 250
 gca cct gcc cag cac ctc gac ccg gag ctg cgc gac cgc atc tgt gcc 1119
 Ala Pro Ala Gln His Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala
 255 260 265
 gat gcc gtg aag ttc tgc aaa tcc atc gga tac cag ggc gcc ggc acc 1167
 Asp Ala Val Lys Phe Cys Lys Ser Ile Gly Tyr Gln Gly Ala Gly Thr
 270 275 280
 gtg gag ttc ctc gtc gac gag gcg ggc aac cac gtc ttc att gag atg 1215
 Val Glu Phe Leu Val Asp Glu Ala Gly Asn His Val Phe Ile Glu Met
 -- 285 290 295
 aac ccc cgc atc cag gtg gaa cac acc gtc acc gag gag gtc acc tcc 1263
 Asn Pro Arg Ile Gln Val Glu His Thr Val Thr Glu Glu Val Thr Ser
 300 305 310 315
 gtc gac ctg gtc aag gcg cag atg cac ctg gcc gcc ggt gcc acc ctg 1311
 Val Asp Leu Val Lys Ala Gln Met His Leu Ala Ala Gly Ala Thr Leu
 320 325 330

aag gaa ctg ggc ctg acc cag gac aag atc acc acc cac ggt gcc gcc	1359
Lys Glu Leu Gly Leu Thr Gln Asp Lys Ile Thr Thr His Gly Ala Ala	
335 340 345	
ctg cag tgc cgc atc acc acg gag gac ccg tcc aac aac ttc cgg ccc	1407
Leu Gln Cys Arg Ile Thr Thr Glu Asp Pro Ser Asn Asn Phe Arg Pro	
- - - 350 - - - 355 - - - 360 - - -	
gac acc ggt gtg atc acc gcc tac cgc tcc ccg ggt ggt gct ggt gtg	1455
Asp Thr Gly Val Ile Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val	
365 370 375	
cgt ctc gac ggc gca gcc cag ctc ggc gag atc acc gca cat ttc	1503
Arg Leu Asp Gly Ala Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe	
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gat tcc atg ctg gtc aag atg acc tgc cgc ggt tcc gat ttc gag acc	1551
Asp Ser Met Leu Val Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr	
400 405 410	
gcc gtg tcc cga gcc cag cgc gcc ctg gcg gag ttc aac gtc tcc ggc	1599
Ala Val Ser Arg Ala Gln Arg Ala Leu Ala Glu Phe Asn Val Ser Gly	
415 420 425	
gtg gcc acc aac atc ggc ttc ctg cgt gcg ctg ctg cgc gag gaa gac	1647
Val Ala Thr Asn Ile Gly Phe Leu Arg Ala Leu Leu Arg Glu Glu Asp	
430 435 440	
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Phe Thr Lys Arg Arg Ile Asp Thr Gly Phe Ile Gly Ser His Gln His	
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Leu Leu Gln Ala Pr Pr Ala Asp Asp Glu Gln Gly Arg Ile Leu Glu	
460 465 470 475	
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Tyr Leu Ala Asp Val Thr Val Asn Lys Pro His Gly Glu Arg Pro Glu	

480	485	490	
aca gcc cgt ccg ata gag aag ctg ccc gag gtg gag aac atc ccg ctg			1839
Thr Ala Arg Pro Ile Glu Lys Leu Pro Glu Val Glu Asn Ile Pro Leu			
495	500	505	
cca cgc ggc tcc cgc gac cgc ctg aag cag ctc ggc ccg gag ggt ttc			1887
Pro Arg Gly Ser Arg Asp Arg Leu Lys Gln Leu Gly Pro Glu Gly Phe			
510	515	520	
gcc cgc gat ctg cgc gaa cag gat gcc ctg gcc gtc acc gac acc acc			1935
Asp Leu Arg Glu Gln Asp Ala Leu Ala Val Thr Asp Thr Thr			
525	530	535	
ttc cgc gat gcc cac cag tcc ctc ctg gcc acc cgc gtg cgc tcc ttc			1983
Phe Arg Asp Ala His Gln Ser Leu Leu Ala Thr Arg Val Arg Ser Phe			
540	545	550	555
gcg ctg acc ccg gcg cgc gcc gtc gca aag ctc acc ccc gag ctg			2031
Ala Leu Thr Pro Ala Ala Arg Ala Val Ala Lys Leu Thr Pro Glu Leu			
560	565	570	
ctg tcg gtg gag gcc tgg ggc ggt gcc acc tac gac gtg gcc atg cgc			2079
Leu Ser Val Glu Ala Trp Gly Gly Ala Thr Tyr Asp Val Ala Met Arg			
575	580	585	
ttc ctc ttc gag gat ccg tgg gca cgc ctg gat gag ctg cgt gag gcg			2127
Phe Leu Phe Glu Asp Pro Trp Ala Arg Leu Asp Glu Leu Arg Glu Ala			
590	595	600	
atg ccg aat gtg aac atc cag atg ctg ctg cgt ggt cgc aac acc gtc			2175
Met Pro Asn Val Asn Ile Gln Met Leu Leu Arg Gly Arg Asn Thr Val			
605	610	615	
ggg tac acc ccg tac ccc gat tcg gtg tgc cgc gcg ttt gtg cag gag			2223
Gly Tyr Thr Pro Tyr Pro Asp Ser Val Cys Arg Ala Phe Val Gln Glu			
620	625	630	635
gcc gcc aag tcc ggt gtg gac atc ttc cgc atc ttc gac gcg ctc aac			2271

Ala Ala Lys Ser Gly Val Asp Ile Phe Arg II Phe Asp Ala Leu Asn
 640 645 650
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 Asp Ile Ser Gln Met Arg Pro Ala Ile Asp Ala Val Leu Glu Thr Gly
 655 660 665
 acc agt gtt gcc gag gtc gcc atg gcg tac tcc ggt gac ctg tcc aat 2367
 Thr Ser Val Ala Glu Val Ala Met Ala Tyr Ser Gly Asp Leu Ser Asn
 670 675 680
 ccg ggg gag aag ctc tac acc ctg gac tac tac ctg aac ctg gcc gag 2415
 Pro Gly Glu Lys Leu Tyr Thr Leu Asp Tyr Tyr Leu Asn Leu Ala Glu
 685 690 695
 cag atc gtc gac tcc ggt gca cac atc ctg gcc atc aag gac atg gcc 2463
 Gln Ile Val Asp Ser Gly Ala His Ile Leu Ala Ile Lys Asp Met Ala
 700 705 710 715
 ggc ctg ctg cgc cgc gcc gcg ccc aaa ctg gtc acc gcc ctg cgc 2511
 Gly Leu Leu Arg Arg Ala Ala Ala Pro Lys Leu Val Thr Ala Leu Arg
 720 725 730
 cgt gaa ttc gac ctg ccc gtg cat gtc cac acc cac gac acc gcc ggc 2559
 Arg Glu Phe Asp Leu Pro Val His Val His Thr His Asp Thr Ala Gly
 735 740 745
 ggt cag ctg gcc acc tac ctg gcc gcc aac gcc ggg gcc gat gcc 2607
 Gly Gln Leu Ala Thr Tyr Leu Ala Ala Ala Asn Ala Gly Ala Asp Ala
 750 755 760
 gtc gac gcc gcc tcc gca ccc ctg tcc ggt acc acc tcc cag ccg tcg 2655
 Val Asp Ala Ala Ser Ala Pro Leu Ser Gly Thr Thr Ser Gln Pro Ser
 765 770 775
 atg tcc gct ctg gtt gcc gcg ttt gcg cac acc cga cgc gac acc ggc 2703
 Met Ser Ala Leu Val Ala Ala Phe Ala His Thr Arg Arg Asp Thr Gly
 780 785 790 795

ctc aac ctg cag gcc gtc tcc gac ctg gaa ccg tac tgg gag gcg gtc 2751
 Leu Asn Leu Gln Ala Val Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val
 800 805 810
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 Arg Gly Leu Tyr Leu Pro Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly
 815 820 825
 cgc gtt tac cgc cac gag atc ccc ggc ggt cag ctg tcc aac ctg cgt 2847
 Arg Val Tyr Arg His Glu Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg
 835 840
 gcc cag gcc gtt gca ctg ggt ctg gcc gac cgc ttc gag ctc atc gag 2895
 Ala Gln Ala Val Ala Leu Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu
 845 850 855
 gac tac tac gcg gcc gtc aac gag atg ctg ggt cgt ccg acc aag gtc 2943
 Asp Tyr Tyr Ala Ala Val Asn Glu Met Leu Gly Arg Pro Thr Lys Val
 860 865 870 875
 acc ccg tcc tcc aag gtt gtc ggt gac ctc gca ctg cac ctc gtc ggt 2991
 Thr Pro Ser Ser Lys Val Val Gly Asp Leu Ala Leu His Leu Val Gly
 880 885 890
 gcc ggt gtg agc ccg gag gat ttc gcc gcc gat ccg cag aag tac gac 3039
 Ala Gly Val Ser Pro Glu Asp Phe Ala Ala Asp Pro Gln Lys Tyr Asp
 895 900 905
 atc ccc gat tcg gtc atc gcc ttc ctc cgc ggc gaa ctg ggt acc cct 3087
 Ile Pro Asp Ser Val Ile Ala Phe Leu Arg Gly Glu Leu Gly Thr Pro
 910 915 920
 ccc ggt ggc tgg ccc gaa ccg ctg cgc acc cgt gca ctc gag ggt cgc 3135
 Pro Gly Gly Trp Pro Glu Pro Leu Arg Thr Arg Ala Leu Glu Gly Arg
 925 930 935
 tcc cag ggt aag gcc ccg ctg gcg gag atc ccc gcc gag gag cag gcc 3183
 Ser Gln Gly Lys Ala Pro Leu Ala Glu Ile Pro Ala Glu Glu Gln Ala

940	945	950	955	
cac ctg gat tcc gat gat tcc gcg gag cgt cgc ggc acc ctc aac cgc				3231
His Leu Asp Ser Asp Asp Ser Ala Glu Arg Arg Gly Thr Leu Asn Arg				
960	965	970		
ctg ctg ttc ccg aag ccg acc gag gag ttc ctt gag cac cgt cgc cgc				3279
Leu-Leu-Phe-Pro-Lys-Pro-Thr-Glu-Glu-Phe-Leu-Glu-His Arg Arg Arg				
975	980	985		
ttc ggc aac acc tcc gcc ctg gat gac cgc gag ttc ttc tac ggc ttg				3327
Phe Gly Asn Thr Ser Ala Leu Asp Asp Arg Glu Phe Phe Tyr Gly Leu				
990	995	1000		
aag gag gga cgt gag gag ctg atc cga ctg acc ggt gtg tcc acc ccg				3375
Lys Glu Gly Arg Glu Glu Leu Ile Arg Leu Thr Gly Val Ser Thr Pro				
1005	1010	1015		
atg gtg gtc cgc ctg gat gcg gtg tcc gaa ccg gat gac aaa ggc atg				3423
Met Val Val Arg Leu Asp Ala Val Ser Glu Pro Asp Asp Lys Gly Met				
1020	1025	1030	1035	
cgc aac gtg gtg gtc aac gtc aac ggc cag atc cgc ccg atc aag gtg				3471
Arg Asn Val Val Val Asn Val Asn Gly Gln Ile Arg Pro Ile Lys Val				
1040	1045	1050		
cgc gac cgt tcc gtg gag tcc gtc acc gcc acc gcg gag aag gcc gat				3519
Arg Asp Arg Ser Val Glu Ser Val Thr Ala Thr Ala Glu Lys Ala Asp				
1055	1060	1065		
gcc acc aac aag ggc cat gtc gcc gca cca ttc gcc ggt gtg gtc acc				3567
Ala Thr Asn Lys Gly His Val Ala Ala Pro Phe Ala Gly Val Val Thr				
1070	1075	1080		
gtg acc gtc gcc gag ggt gat ga~ atc aag gct ggc gac gcc gtg gcc				3615
Val Thr Val Ala Glu Gly Asp Glu Ile Lys Ala Gly Asp Ala Val Ala				
1085	1090	1095		
atc att gag gcc atg aag atg gag gcc acc atc acc gcg cct gtc gac				3663

Ile Ile Glu Ala Met Lys Met Glu Ala Thr Ile Thr Ala Pro Val Asp
 1100 1105 1110 1115
 ggt gtc atc gac cgc gtc gtg gtg ccc gcc acc aag gtc gag ggc 3711
 Gly Val Ile Asp Arg Val Val Val Pro Ala Ala Thr Lys Val Glu Gly
 1120 1125 1130
 ggc-gac-ctc-atc gtg gtc-gtg-tcc-tagcgactga-gagccacaac ccgtccccggg—3765
 Gly Asp Leu Ile Val Val Val Ser
 1135
 ..
 tgccctttta tcaaccctccc ccttgtatgtt ttcctcagggg gaggctctac gtacctcacc 3825
 gtgacgggtgc atgtatatcg tcctgctggaa gagaatgcgc caggttaggaa cgccaaaccac 3885
 cccactccgt gatgtcccggt gctgatccca ggcaggccgg ttggaaagaa aaaccagtga 3945
 tggaacggcc atcggacagc gagacggaac caagcgtcat cggctccgggt agagcggta 4005
 ggagcctg 4013

[0090]

<210> 24

<211> 1139

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 24

Val Val Thr Thr Thr Pro Ser Thr Leu Pro Ala Phe Lys Lys Ile Leu

1 5 10 15

Val Ala Asn Arg Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala Tyr

20 25 30

Glu Thr Gly Ala Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg Gly

35 40 45

Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr Glu

50 55 60

Gly Ser Pr Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Asn Ala

65 70 75 80

Ala Lys Lys Val Lys Ala Asp Ala Val Tyr Pro Gly Tyr Gly Phe Leu
 85 90 95
 Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr
 100 105 110
 Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys Ser
 115 120 125
 Lys Ala Val Ser Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala Glu
 130 135 140
 Ser Thr Pro Ser Thr Asp Ile Asp Glu Ile Val Lys Ser Ala Glu Gly
 145 150 155 160
 Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Arg
 165 170 175
 Gly Met Arg Phe Val Glu Lys Pro Glu Asp Leu Arg Glu Leu Ala Arg
 180 185 190
 Glu Ala Ser Arg Glu Ala Glu Ala Phe Gly Asp Gly Ser Val Tyr
 195 200 205
 Val Glu Arg Ala Val Ile Lys Pro Gln His Ile Glu Val Gln Ile Leu
 210 215 220
 Gly Asp His Thr Gly Asp Val Ile His Leu Tyr Glu Arg Asp Cys Ser
 225 230 235 240
 Leu Gln Arg Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln His
 245 250 255
 Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys Phe
 260 265 270
 Cys Lys Ser Ile Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu Val
 275 280 285
 Asp Glu Ala Gly Asn His Val Phe Ile Glu Met Asn Pr Arg Ile Gln
 290 295 300
 Val Glu His Thr Val Thr Glu Glu Val Thr Ser Val Asp Leu Val Lys

305	310	315	320
Ala Gln Met His Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu			
325	330	335	
Thr Gln Asp Lys Ile Thr Thr His Gly Ala Ala Leu Gln Cys Arg Ile			
340	345	350	
Thr Thr Glu-Asp Pro Ser Asn Asn-Phe Arg Pro Asp Thr-Gly Val Ile			
355	360	365	
Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly Ala			
		380	
Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu Val			
385	390	395	400
Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr Ala Val Ser Arg Ala			
405	410	415	
Gln Arg Ala Leu Ala Glu Phe Asn Val Ser Gly Val Ala Thr Asn Ile			
420	425	430	
Gly Phe Leu Arg Ala Leu Leu Arg Glu Glu Asp Phe Thr Lys Arg Arg			
435	440	445	
Ile Asp Thr Gly Phe Ile Gly Ser His Gln His Leu Leu Gln Ala Pro			
450	455	460	
Pro Ala Asp Asp Glu Gln Gly Arg Ile Leu Glu Tyr Leu Ala Asp Val			
465	470	475	480
Thr Val Asn Lys Pro His Gly Glu Arg Pro Glu Thr Ala Arg Pro Ile			
485	490	495	
Glu Lys Leu Pro Glu Val Glu Asn Ile Pro Leu Pro Arg Gly Ser Arg			
500	505	510	
Asp Arg Leu Lys Gln Leu Gly Pro Glu Gly Phe Ala Arg Asp Leu Arg			
515	520	525	
Glu Gln Asp Ala Leu Ala Val Thr Asp Thr Thr Phe Arg Asp Ala His			
530	535	540	

Gln Ser Leu Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Thr Pro Ala
 545 550 555 560
 Ala Arg Ala Val Ala Lys Leu Thr Pro Glu Leu Leu Ser Val Glu Ala
 565 570 575
 Trp Gly Gly Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu Asp
 580 585 590
 Pro Trp Ala Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn
 595 600 605
 Ile Un Met Leu Asp Ala Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr
 610 615 620
 Pro Asp Ser Val Cys Arg Ala Phe Val Gln Glu Ala Ala Lys Ser Gly
 625 630 635 640
 Val Asp Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Ile Ser Gln Met
 645 650 655
 Arg Pro Ala Ile Asp Ala Val Leu Glu Thr Gly Thr Ser Val Ala Glu
 660 665 670
 Val Ala Met Ala Tyr Ser Gly Asp Leu Ser Asn Pro Gly Glu Lys Leu
 675 680 685
 Tyr Thr Leu Asp Tyr Tyr Leu Asn Leu Ala Glu Gln Ile Val Asp Ser
 690 695 700
 Gly Ala His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Arg
 705 710 715 720
 Ala Ala Ala Pro Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu
 725 730 735
 Pro Val His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr
 740 745 750
 Tyr Leu Ala Ala Ala Asn Ala Gly Ala Asp Ala Val Asp Ala Ala Ser
 755 760 765
 Ala Pro Leu Ser Gly Thr Thr Ser Gln Pr Ser Met Ser Ala Leu Val

770

775

780

Ala Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Asn Leu Gln Ala

785

790

795

800

Val Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu

805

810

815

—Pro-Phe-Glu-Ser-Gly-Thr-Pro-Gly-Pro-Thr-Gly-Arg-Val-Tyr-Arg-His—

820

825

830

Glu Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Val Ala

835

845

Leu Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Tyr Tyr Ala Ala

850

855

860

Val Asn Glu Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys

865

870

875

880

Val Val Gly Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Ser Pro

885

890

895

Glu Asp Phe Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val

900

905

910

Ile Ala Phe Leu Arg Gly Glu Leu Gly Thr Pro Pro Gly Gly Trp Pro

915

920

925

Glu Pro Leu Arg Thr Arg Ala Leu Glu Gly Arg Ser Gln Gly Lys Ala

930

935

940

Pro Leu Ala Glu Ile Pro Ala Glu Glu Gln Ala His Leu Asp Ser Asp

945

950

955

960

Asp Ser Ala Glu Arg Arg Gly Thr Leu Asn Arg Leu Leu Phe Pro Lys

965

970

975

Pro Thr Glu Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser

980

985

990

Ala Leu Asp Asp Arg Glu Phe Phe Tyr Gly Leu Lys Glu Gly Arg Glu

995

1000

1005

Glu Leu Ile Arg Leu Thr Gly Val Ser Thr Pro Met Val Val Arg Leu
 1010 1015 1020
 Asp Ala Val Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Val
 025 1030 1035 1040
 Asn Val Asn Gly Gln Ile Arg Pro Ile Lys Val Arg Asp Arg Ser Val
 1045 1050 1055
 Glu Ser Val Thr Ala Thr Ala Glu Lys Ala Asp Ala Thr Asn Lys Gly
 1060 1065 1070
 His Val Ala Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu
 1075 1080 1085
 Gly Asp Glu Ile Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met
 1090 1095 1100
 Lys Met Glu Ala Thr Ile Thr Ala Pro Val Asp Gly Val Ile Asp Arg
 105 1110 1115 1120
 Val Val Val Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile Val
 1125 1130 1135
 Val Val Ser

【0091】

<210> 25
 <211> 3306
 <212> DNA
 <213> *Corynebacterium thermoaminogenes*

<220>
 <221> CDS
 <222> (64)..(2820)

<400> 25

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 acc gtg aat gaa ctt ctc cgt gac gat atc cgt tat ctc ggc cgg atc 108
 Val Asn Glu Leu Leu Arg Asp Asp Ile Arg Tyr Leu Gly Arg Ile
 1 5 10 15
 ctg ggc gag gtg atc tcc gag cag gag ggc cac cat gtc ttc gaa ctg 156
 Leu Gly Glu Val Ile Ser Glu Gln Glu Gly His His Val Phe Glu Leu
 20 25 30
 gtt gaa cgc gcc cgc cgg acc tcc ttc gac atc gcc aag gga cgc gcg 204
 Val Glu Arg Ala Arg Arg Thr Ser Phe Asp Ile Ala Lys Gly Arg Ala
 35 40 45
 gag atg gac agt ctg gtg gag gtg ttc gct ggc atc gac ccg gag gac 252
 Glu Met Asp Ser Leu Val Glu Val Phe Ala Gly Ile Asp Pro Glu Asp
 50 - - - - - 55 60
 gcc acg ccc gtg gcc cga gcc ttc acc cat ttc gcc ctg ttg gcc aac 300
 Ala Thr Pro Val Ala Arg Ala Phe Thr His Phe Ala Leu Leu Ala Asn
 65 70 75
 ctc gcg gag gat ttg cat gac gca gcc cag cgg gaa cag gcc ctg aac 348
 Leu Ala Glu Asp Leu His Asp Ala Ala Gln Arg Glu Gln Ala Leu Asn
 80 85 90 95
 tcg ggt gag ccc gcg ccg gac agc acc ctc gag gcc acc tgg gtg aaa 396
 Ser Gly Glu Pro Ala Pro Asp Ser Thr Leu Glu Ala Thr Trp Val Lys
 100 105 110
 ctg gat gat gcc ggg gtg ggc agc ggt gag gtc gcc gcg gtg atc cgc 444
 Leu Asp Asp Ala Gly Val Gly Ser Gly Glu Val Ala Ala Val Ile Arg
 115 120 125
 aat gcg ctc gtc gcc ccg gtg ctc acc gcg cac ccg acg gaa acc cga 492
 Asn Ala Leu Val Ala Pro Val Leu Thr Ala His Pr Thr Glu Thr Arg
 130 135 140
 cgt cgt acc gtg ttc gac gcg cag aag cac atc acc gcc ctg atg gag 540

Arg Arg Thr Val Phe Asp Ala Gln Lys His Ile Thr Ala Leu Met Glu

145 150 155

gaa cgc cac ctc ctc ctg gcg ctg ccc acg cat gcc cgg acc cag tcc 588

Glu Arg His Leu Leu Leu Ala Leu Pro Thr His Ala Arg Thr Gln Ser.

160 165 170 175

aag ctg gat gac atc gag ege aac atc cgg ega cgg atc acg atc ctg 636

Lys Leu Asp Asp Ile Glu Arg Asn Ile Arg Arg Arg Ile Thr Ile Leu

180 185 190

tgg cag acg gcc ctc atc cgt gtg gcc cgt ccc cgc atc gag gat gag 684

Trp Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg Ile Glu Asp Glu

195 200 205

gtc gag gtt gga ctg cgc tac tac aag ctc agc ctg ttg gcc gag atc 732

Val Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu Leu Ala Glu Ile

210 215 220

ccc cgc atc aat cat gat gtg acc acc gtg gaa ctg gcc cgg cgt ttc ggc 780

Pro Arg Ile Asn His Asp Val Thr Val Glu Leu Ala Arg Arg Phe Gly

225 230 235

ggg gat atc ccc acc acg gcg atg gtc agg ccg gga tcc tgg atc ggc 828

Gly Asp Ile Pro Thr Thr Ala Met Val Arg Pro Gly Ser Trp Ile Gly

240 245 250 255

ggg gac cat gat ggc aac ccc ttc gtc acc gcg gag act gtc acc tac 876

Gly Asp His Asp Gly Asn Pro Phe Val Thr Ala Glu Thr Val Thr Tyr

260 265 270

gcc acc cat cgg gcc gcg gag acc gtg ctc aag tac tac gtc aag caa 924

Ala Thr His Arg Ala Ala Glu Thr Val Leu Lys Tyr Tyr Val Lys Gln

275 280 285

ctg cac gcc ctg gaa cac gaa ctc agt ctc tcc gac cgg atg aac gtc 972

L u His Ala Leu Glu His Glu Leu Ser Leu Ser Asp Arg Met Asn Val

290 295 300

atc agc gat gag ctg cgt gtg ctt gcc gat gcc ggc cag aat gac atg 1020
 Ile S r Asp Glu Leu Arg Val Leu Ala Asp Ala Gly Gln Asn Asp Met
 305 310 315
 ccc agc cgg gtt gat gaa ccc tac cgg cgg gcc atc cac ggc atg cgt 1068
 Pro Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Ile His Gly Met Arg
 320 325 330 335
 ggc cgg atg ctg gcc acc acg gcc ctc atc ggt gag gag gcg gtc 1116
 Gly Arg Met Leu Ala Thr Thr Ala Ala Leu Ile Gly Glu Glu Ala Val
 340 345 350
 gag ggc acc tgg ttc aag acc ttc acg ccc tat acc gat acc cac gag 1164
 Glu Gly Thr Trp Phe Lys Thr Phe Thr Pro Tyr Thr Asp Thr His Glu
 355 360 365
 ttc aaa cgc gac ctc gat atc gtc gat ggt tcc ctc aga atg tcc cgg 1212
 Phe Lys Arg Asp Leu Asp Ile Val Asp Gly Ser Leu Arg Met Ser Arg
 370 375 380
 gat gac atc atc gcc gat gac cgt ctc gtc atg ctc cgc tcg gcc ctc 1260
 Asp Asp Ile Ile Ala Asp Asp Arg Leu Ala Met Leu Arg Ser Ala Leu
 385 390 395
 gac agc ttc ggg ttc aac ctc tac tcc ctc gat ctc cgc cag aat tcc 1308
 Asp Ser Phe Gly Phe Asn Leu Tyr Ser Leu Asp Leu Arg Gln Asn Ser
 400 405 410 415
 gac ggt ttc gag gat gtc ctc acc gaa ttg ttc gcc acc gcc cag acc 1356
 Asp Gly Phe Glu Asp Val Leu Thr Glu Leu Phe Ala Thr Ala Gln Thr
 420 425 430
 gag aag aac tac cgc ggg ttg acg gag gcg gag aag ctc gac ctc ctc 1404
 Glu Lys Asn Tyr Arg Gly Leu Thr Glu Ala Glu Lys Leu Asp Leu Leu
 435 440 445
 atc cgc gaa ctc agc aca ccc cgc ccg ctc atc ccg cac ggg gac ccg 1452
 Ile Arg Glu Leu Ser Thr Pr Arg Pr Leu Ile Pr His Gly Asp Pr

450	455	460	
gac tac tcc gag gcc acc aac cgt gaa ctg ggg att ttt tcg aag gcc			1500
Asp Tyr Ser Glu Ala Thr Asn Arg Glu Leu Gly Ile Phe Ser Lys Ala			
465	470	475	
gcg gag gcc gtg cgt aaa ttc ggt cct ctc atg gtg ccg cac tgc atc			1548
Ala Glu Ala Val Arg Lys Phe Gly Pro Leu Met Val Pro His Cys Ile			
480	485	490	495
atc tcc atg gcc tct tcc gtc acg gac atc ctc gaa ccg atg gtg ctg			1596
Ile Ser Met Ala Ser Ser Val Thr Asp Ile Leu Glu Pro Met Val Leu			
500	505	510	
ctc aag gag ttc ggt ctg atc cgg gcc aac ggg aag aac ccg acg ggc			1644
Leu Lys Glu Phe Gly Leu Ile Arg Ala Asn Gly Lys Asn Pro Thr Gly			
515	520	525	
agc gtc gac gtg atc ccg ctg ttc gag acg atc gat gac ctc cag cgt			1692
Ser Val Asp Val Ile Pro Leu Phe Glu Thr Ile Asp Asp Leu Gln Arg			
530	535	540	
ggc gcg ggc atc ctg gag gaa ttg tgg gac atc gac ctc tac cgc aat			1740
Gly Ala Gly Ile Leu Glu Glu Leu Trp Asp Ile Asp Leu Tyr Arg Asn			
545	550	555	
tac ctt gag cag cgg gac aac gtc cag gag gtc atg ctg ggg tat tcc			1788
Tyr Leu Glu Gln Arg Asp Asn Val Gln Glu Val Met Leu Gly Tyr Ser			
560	565	570	575
gac tcc aac aag gac ggc ggg tac ttc gcc gcc aac tgg gcg ctt tac			1836
Asp Ser Asn Lys Asp Gly Gly Tyr Phe Ala Ala Asn Trp Ala Leu Tyr			
580	585	590	
gac gcg gag tta cgc ctg gtc gaa cta tgc cgg ggc cgt aat gtc aag			1884
Asp Ala Glu Leu Arg Leu Val Glu Leu Cys Arg Gly Arg Asn Val Lys			
595	600	605	
ctc cgt ctc ttc cac ggt cgt ggt ggc acg gtg ggt cgt ggc ggt ggc			1932

Leu Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly Arg Gly Gly Gly
 610 615 620
 ccc tcc tat gat gcg atc ctg gcc cag ccc aag ggc ggc gtc cg^c ggt 1980
 Pro Ser Tyr Asp Ala Ile Leu Ala Gln Pro Lys Gly Ala Val Arg Gly
 625 630 635
 gcg gtg cgg gtg act gaa cag ggc gag atc atc tcc gcg aag tac ggt 2028
 Ala Val Arg Val Thr Glu Gln Gly Glu Ile Ile Ser Ala Lys Tyr Gly
 640 645 650 655
 aac ccg gat acg gca cgc cgc aac ctt gag gcc ctg gtg tcc gcg acg 2076
 Asn Pro Asp Thr Ala Arg Arg Asn Leu Glu Ala Leu Val Ser Ala Thr
 660 665 670
 ctg gag gca tcg ctt ctg gat gat gtg gaa ctg ccc aat cgg gaa cgc 2124
 Leu Glu Ala Ser Leu Leu Asp Asp Val Glu Leu Pro Asn Arg Glu Arg
 675 680 685
 gcg cac cag atc atg ggg gag atc tcg gag ttg agc ttc cgc agg tac 2172
 Ala His Gln Ile Met Gly Glu Ile Ser Glu Leu Ser Phe Arg Arg Tyr
 690 695 700
 tca tca ctg gtc cat gag gat ccc gga ttc atc cag tac ttc acc cag 2220
 Ser Ser Leu Val His Glu Asp Pro Gly Phe Ile Gln Tyr Phe Thr Gln
 705 710 715
 tcc acc ccc ctg cag gag atc gga tcc ctc aac atc ggt tcc cga ccc 2268
 Ser Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile Gly Ser Arg Pro
 720 725 730 735
 tcc tca cgt aaa cag acc aac acg gtg gag gat ctg cgt gcc atc ccg 2316
 Ser Ser Arg Lys Gln Thr Asn Thr Val Glu Asp Leu Arg Ala Ile Pro
 740 745 750
 tgg gtg ctc agc tgg tcc cag tcc cgt gtc atg ctg ccg ggc tgg ttc 2364
 Trp Val L u Ser Trp Ser Gln Ser Arg Val Met Leu Pro Gly Trp Phe
 755 760 765

ggt gtg ggt acc gca ctg cgt gag tgg atc ggt gag ggg gag ggg gct 2412
 Gly Val Gly Thr Ala L u Arg Glu Trp Ile Gly Glu Gly Glu Ala
 770 775 780
 gcg gag cgc atc gcg gag ctg cag gaa ctc aac cgg tgc tgg ccg ttc 2460
 Ala Glu Arg Ile Ala Glu Leu Gln Glu Leu Asn Arg Cys Trp Pro Phe
 785 790 795
 ttc acc tcg gtg ctg gac aac atg gcc cag gtg atg agc aag gcg gaa 2508
 Phe Thr Ser Val Leu Asp Asn Met Ala Gln Val Met Ser Lys Ala Glu
 800 805 810
 ctg cgc ctg gcc agg ttg tac gcc gat ctc atc ccg gat cgc gag gtg 2556
 Leu Arg Leu Ala Arg Leu Tyr Ala Asp Leu Ile Pro Asp Arg Glu Val
 820 825 830
 gcg gac cgg atc tat gag acc atc ttc ggg gag tat ttc ctg acc aag 2604
 Ala Asp Arg Ile Tyr Glu Thr Ile Phe Gly Glu Tyr Phe Leu Thr Lys
 835 840 845
 gag atg ttc tgc acc atc acc ggt tcc cag gac ctg ctc gat gac aac 2652
 Glu Met Phe Cys Thr Ile Thr Gly Ser Gln Asp Leu Leu Asp Asp Asn
 850 855 860
 ccg gcg ctg gcg cga tcg gtg cgc agt cgg ttc ccg tac ctg ctg ccg 2700
 Pro Ala Leu Ala Arg Ser Val Arg Ser Arg Phe Pro Tyr Leu Leu Pro
 865 870 875
 ctc aat gtc atc cag gtg gag atg atg cgc cgg tac cgg tcc ggt gat 2748
 Leu Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr Arg Ser Gly Asp
 880 885 890 895
 gag ggc acg gct gtc cca cgt aat atc cgc ctg acc atg aat gga ttg 2796
 Glu Gly Thr Ala Val Pro Arg Asn Ile Arg Leu Thr Met Asn Gly Leu
 900 905 910
 tcc acg gcc ctg cgc aac tcg ggt tagggcgcca gacgccccgg gaacccgcac 2850
 Ser Thr Ala Leu Arg Asn Ser Gly

915

cctgtgtata ctgtctaaag ttgcccggtg tcatccgggc gtgatggata gacaacttaa 2910
 cggcaaaggaa ttctccccac atggcaactga cgcttcaaata cgccctcggt ctcgccagcg 2970
 tgctcaitgac ggcttcgcgc ctgctgcaca agggtaaggg cggaggctgt tcaagcctct 3030
 tcggtggtgg cgtccagtc aacctctccg gttccacgggt ggtggagaag aacctggacc 3090
 gcgtcaccat cctgaccgca gtcatctgggt tgatctgcat tgtcgcgctc aacctcatcc 3150
 aggctactc ctagcacctg atcttcaag gcctgcccctt cggggcaggc ctttttgca 3210
 ttctccaggt gatgtccatc acccaccgggt tttaaactat tgaccgatag aaacacctgc 3270
 aciaggttat cigitaitgca atagaaaata gtgcatt 3306

【0092】

<210> 26

<211> 919

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 26

Val Asn Glu Leu Leu Arg Asp Asp Ile Arg Tyr Leu Gly Arg Ile Leu				
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Gly Glu Val Ile Ser Glu Gln Glu Gly His His Val Phe Glu Leu Val				
20	25	30		
Glu Arg Ala Arg Arg Thr Ser Phe Asp Ile Ala Lys Gly Arg Ala Glu				
35	40	45		
Met Asp Ser Leu Val Glu Val Phe Ala Gly Ile Asp Pro Glu Asp Ala				
50	55	60		
Thr Pro Val Ala Arg Ala Phe Thr His Phe Ala Leu Leu Ala Asn Leu				
65	70	75	80	
Ala Glu Asp Leu His Asp Ala Ala Gln Arg Glu Gln Ala Leu Asn Ser				
85	90	95		
Gly Glu Pr Ala Pro Asp Ser Thr Leu Glu Ala Thr Trp Val Lys Leu				

100	105	110
Asp Asp Ala Gly Val Gly Ser Gly Glu Val Ala Ala Val Ile Arg Asn		
115	120	125
Ala Leu Val Ala Pro Val Leu Thr Ala His Pro Thr Glu Thr Arg Arg		
130	135	140
Arg Thr Val Phe Asp Ala Gln Lys His Ile Thr Ala Leu Met Glu Glu		
145	150	155
160		
Arg His Leu Leu Leu Ala Leu Pro Thr His Ala Arg Thr Gln Ser Lys		
165	170	175
Leu Asp Asp Ile Glu Arg Asn Ile Arg Arg Arg Ile Thr Ile Leu Trp		
180	185	190
Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg Ile Glu Asp Glu Val		
195	200	205
Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu Leu Ala Glu Ile Pro		
210	215	220
Arg Ile Asn His Asp Val Thr Val Glu Leu Ala Arg Arg Phe Gly Gly		
225	230	235
240		
Asp Ile Pro Thr Thr Ala Met Val Arg Pro Gly Ser Trp Ile Gly Gly		
245	250	255
Asp His Asp Gly Asn Pro Phe Val Thr Ala Glu Thr Val Thr Tyr Ala		
260	265	270
Thr His Arg Ala Ala Glu Thr Val Leu Lys Tyr Tyr Val Lys Gln Leu		
275	280	285
His Ala Leu Glu His Glu Leu Ser Leu Ser Asp Arg Met Asn Val Ile		
290	295	300
Ser Asp Glu Leu Arg Val Leu Ala Asp Ala Gly Gln Asn Asp Met Pro		
305	310	315
320		
Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Ile His Gly M t Arg Gly		
325	330	335

Arg Met Leu Ala Thr Thr Ala Ala Leu Ile Gly Glu Glu Ala Val Glu
 340 345 350
 Gly Thr Trp Phe Lys Thr Phe Thr Pro Tyr Thr Asp Thr His Glu Phe
 355 360 365
 Lys Arg Asp Leu Asp Ile Val Asp Gly Ser Leu Arg Met Ser Arg Asp
 370 375 380
 Asp Ile Ile Ala Asp Asp Arg Leu Ala Met Leu Arg Ser Ala Leu Asp
 385 390 395 400
 Ser Phe Gly Phe Asn Leu Tyr Ser Leu Asp Leu Arg Gln Asn Ser Asp
 405 410 415
 Gly Phe Glu Asp Val Leu Thr Glu Leu Phe Ala Thr Ala Gln Thr Glu
 420 425 430
 Lys Asn Tyr Arg Gly Leu Thr Glu Ala Glu Lys Leu Asp Leu Leu Ile
 435 440 445
 Arg Glu Leu Ser Thr Pro Arg Pro Leu Ile Pro His Gly Asp Pro Asp
 450 455 460
 Tyr Ser Glu Ala Thr Asn Arg Glu Leu Gly Ile Phe Ser Lys Ala Ala
 465 470 475 480
 Glu Ala Val Arg Lys Phe Gly Pro Leu Met Val Pro His Cys Ile Ile
 485 490 495
 Ser Met Ala Ser Ser Val Thr Asp Ile Leu Glu Pro Met Val Leu Leu
 500 505 510
 Lys Glu Phe Gly Leu Ile Arg Ala Asn Gly Lys Asn Pro Thr Gly Ser
 515 520 525
 Val Asp Val Ile Pro Leu Phe Glu Thr Ile Asp Asp Leu Gln Arg Gly
 530 535 540
 Ala Gly Ile Leu Glu Glu Leu Trp Asp Ile Asp Leu Tyr Arg Asn Tyr
 545 550 555 560
 Leu Glu Gln Arg Asp Asn Val Gln Glu Val Met Leu Gly Tyr Ser Asp

565	570	575
Ser Asn Lys Asp Gly Gly Tyr Phe Ala Ala Asn Trp Ala Leu Tyr Asp		
580	585	590
Ala Glu Leu Arg Leu Val Glu Leu Cys Arg Gly Arg Asn Val Lys Leu		
595	600	605
Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly Arg Gly Gly Pro		
610	615	620
Ser Tyr Asp Ala Ile Leu Ala Gln Pro Lys Gly Ala Val Arg Gly Ala		
625	630	635
Val Arg Val Thr Glu Gln Gly Glu Ile Ile Ser Ala Lys Tyr Gly Asn		640
645	650	655
Pro Asp Thr Ala Arg Arg Asn Leu Glu Ala Leu Val Ser Ala Thr Leu		
660	665	670
Glu Ala Ser Leu Leu Asp Asp Val Glu Leu Pro Asn Arg Glu Arg Ala		
675	680	685
His Gln Ile Met Gly Glu Ile Ser Glu Leu Ser Phe Arg Arg Tyr Ser		
690	695	700
Ser Leu Val His Glu Asp Pro Gly Phe Ile Gln Tyr Phe Thr Gln Ser		
705	710	715
Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile Gly Ser Arg Pro Ser		720
725	730	735
Ser Arg Lys Gln Thr Asn Thr Val Glu Asp Leu Arg Ala Ile Pro Trp		
740	745	750
Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu Pro Gly Trp Phe Gly		
755	760	765
Val Gly Thr Ala Leu Arg Glu Trp Ile Gly Glu Gly Glu Gly Ala Ala		
770	775	780
Glu Arg Ile Ala Glu Leu Gln Glu Leu Asn Arg Cys Trp Pro Phe Phe		
785	790	795
		800

Thr Ser Val Leu Asp Asn Met Ala Gln Val Met Ser Lys Ala Glu Leu
810 815

Arg Leu Ala Arg Leu Tyr Ala Asp Leu Ile Pro Asp Arg Glu Val Ala
820 825 830

Asp Arg Ile Tyr Glu Thr Ile Phe Gly Glu Tyr Phe Leu Thr Lys Glu
— 835 — 840 — 845 —

Met Phe Cys Thr Ile Thr Gly Ser Gln Asp Leu Leu Asp Asp Asn Pro
 850 855 860

Ala Leu Ala Arg Ser Val Arg Ser Arg Phe Pro Tyr Leu Leu Pro Leu
865 870 875 880

Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr Arg Ser Gly Asp Glu
885 890 895

Gly Thr Ala Val Pro Arg Asn Ile Arg Leu Thr Met Asn Gly Leu Ser
900 905 910

Thr Ala Leu Arg Asn Ser Gly

915

[0093]

<210> 27

211 3907

<212> DNA

<213> *Corynebacterium thermoaminogenes*

220

<221> CDS

<222> (686)..(3388)

<400> 27

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ttattattag ctggtggcgg agatggaact aaagctctca acgcaattca gagtgccgct 180
 attattagtg cgtttccatt ctccttgcgt gtcataattaa tgcataatcg tttctacaaa 240
 gatgctaata aagaacgtaa attcttagga ttaacattaa cgcctaataa acacagatta 300
 gaagaatacg ttaaatatca acaagaggat tacgaatctg atatttaga aaaacgtgaa 360
 tctagacgta atcgtgaaag agaagaataa ttgaatgaaa tatctactat aatggtggt 420
 ttaaagctat caacaatttt gttgatagct attttatgt ttcaaacata taaatattat 480
 ttacttgcga ttgataacca ttctcaatta ataaaaataa cttatagttac aaatgcgtt 540
 taataagtt tacttatact acctgattaa aaatgcgaaa tgaaaaatga ccccttata 600
 tacctataca gtttgtttcg aaaacataata ataaatacaat taaactaagg caataaaata 660
 tatagaaatt caagggggat atcaa atg gct tct aat ttt aaa gaa aca gcg 712

Met Ala Ser Asn Phe Lys Glu Thr Ala

1 5

aag aaa caa ttt gat tta aat ggc caa tca tac acg tac tat gat tta 760

Lys Lys Gln Phe Asp Leu Asn Gly Gln Ser Tyr Thr Tyr Tyr Asp Leu

10 15 20 25

aaa tca tta gaa gaa caa ggt tta act aaa att tca aag tta cct tat 808

Lys Ser Leu Glu Glu Gln Gly Leu Thr Lys Ile Ser Lys Leu Pro Tyr

30 35 40

tca atc cgt gta tta cta gaa tca gtg tta cgt cag gaa gat gat ttt 856

Ser Ile Arg Val Leu Leu Glu Ser Val Leu Arg Gln Glu Asp Asp Phe

45 50 55

gta att act gat gat cac att aaa caa tta gca gaa ttt ggc aaa aaa 904

Val Ile Thr Asp Asp His Ile Lys Gln Leu Ala Glu Phe Gly Lys Lys

60 65 70

ggt aac gaa ggt gaa gta cct ttc aaa cca tct cga gtt att tta caa 952

Gly Asn Glu Gly Glu Val Pro Phe Lys Pro Ser Arg Val Ile Leu Gln

75 80 85

gac ttc act ggt gta cca gca gta gtt gac tta gcg tct tta cgt aaa 1000

Asp Phe Thr Gly Val Pro Ala Val Val Asp Leu Ala Ser Leu Arg Lys

90	95	100	105	
gca atg aat gat gtt ggt ggg gat att aat aaa att aac cct gaa gta				1048
Ala Met Asn Asp Val Gly Gly Asp Ile Asn Lys Ile Asn Pro Glu Val				
110		115		120
cca gtt gac tta gtt att gac cac tct gta caa gta gat agt tat gct				1096
Pro-Val Asp Leu Val Ile Asp His Ser Val Gln-Val Asp Ser Tyr Ala				
125		130		135
aat cca gat gca tta caa cgt aac atg aaa tta gaa ttt gaa cgt aac				1144
Asn Pro Asp Ala Leu Gln Arg Asn Met Lys Leu Glu Phe Glu Arg Asn				
140		145		150
tat gaa cgt tac caa ttc tta aac tgg gca aca aaa gca ttt gat aac				1192
Tyr Glu Arg Tyr Gln Phe Leu Asn Trp Ala Thr Lys Ala Phe Asp Asn				
155		160		165
tat aat gca gta cca cct gct aca ggt att gtc cac caa gta aac tta				1240
Tyr Asn Ala Val Pro Pro Ala Thr Gly Ile Val His Gln Val Asn Leu				
170		175		180
170 gaa tac tta gcg aat gtt gta cat gtt cgt gac gtt gac gga gaa caa				1288
Glu Tyr Leu Ala Asn Val Val His Val Arg Asp Val Asp Gly Glu Gln				
190		195		200
act gct ttc cca gat aca tta gtt ggt act gac tca cat act aca atg				1336
Thr Ala Phe Pro Asp Thr Leu Val Gly Thr Asp Ser His Thr Thr Met				
205		210		215
att aac ggt att ggt gta tta ggt tgg ggt gtc ggc ggt atc gaa gct				1384
Ile Asn Gly Ile Gly Val Leu Gly Trp Gly Val Gly Ile Glu Ala				
220		225		230
gaa gca ggt atg tta gga caa cca tca tac ttc cca att cca gaa gtt				1432
Glu Ala Gly Met Leu Gly Gln Pro Ser Tyr Phe Pro Ile Pr Glu Val				
235		240		245
att ggt gtt aaa tta agt aat gaa tta cca caa ggt tca aca gca act				1480

Ile Gly Val Lys Leu Ser Asn Glu Leu Pro Gln Gly Ser Thr Ala Thr
 250 255 260 265
 gac tta gca tta cgt gta act gaa gag tta cgt aaa cgt ggt gta gta 1528
 Asp Leu Ala Leu Arg Val Thr Glu Glu Leu Arg Lys Arg Gly Val Val
 270 275 280
 ggt aaa ttc gtt gag ttc ttt ggt cct ggt gta aca aac tta cca tta 1576
 Gly Lys Phe Val Glu Phe Phe Gly Pro Gly Val Thr Asn Leu Pro Leu
 285 290 295
 gct gac cgt gca aca att gcg aac atg gcg cct gaa tat ggt gca act 1624
 Ala Asp Arg Ala Thr Ile Ala Asn Met Ala Pro Glu Tyr Gly Ala Thr
 300 305 310
 tgt ggt ttc ttc cca gtt gat gaa gaa tca ctt aaa tac atg aaa tta 1672
 Cys Gly Phe Phe Pro Val Asp Glu Glu Ser Leu Lys Tyr Met Lys Leu
 315 320 325
 act ggt cgt aaa gat gat cat att gca cta gta aaa gaa tat tta caa 1720
 Thr Gly Arg Lys Asp Asp His Ile Ala Leu Val Lys Glu Tyr Leu Gln
 330 335 340 345
 caa aat aat atg ttc ttc caa gtt gaa aat gaa gat cct gaa tat act 1768
 Gln Asn Asn Met Phe Phe Gln Val Glu Asn Glu Asp Pro Glu Tyr Thr
 350 355 360
 gaa gtg att gat tta gat tta tct aca gtt caa gct tct tta tca ggt 1816
 Glu Val Ile Asp Leu Asp Leu Ser Thr Val Gln Ala Ser Leu Ser Gly
 365 370 375
 cca aaa cgt cca caa gat tta atc ttc tta agt gac atg aaa act gaa 1864
 Pro Lys Arg Pro Gln Asp Leu Ile Phe Leu Ser Asp Met Lys Thr Glu
 380 385 390
 ttc gaa aaa tca gtt aca gca cca gct ggt aac caa ggt cac ggt tta 1912
 Phe Glu Lys Ser Val Thr Ala Pro Ala Gly Asn Gln Gly His Gly Leu
 395 400 405

gat gaa agt gaa ttt gat aag aaa gca gaa atc aaa ttt aat gat ggt 1960
 Asp Glu Ser Glu Phe Asp Lys Lys Ala Glu Ile Lys Phe Asn Asp Gly
 410 415 420 425
 aga act tca act atg aag act ggt gat gtt gcg att gca gcg att aca 2008
 Arg Thr Ser Thr Met Lys Thr Gly Asp Val Ala Ile Ala Ala Ile Thr
 430 435 440
 tca tgt aca aat aca tct aac cct tac gtt atg tta ggt gca ggt tta 2056
 Ser Cys Thr Asn Thr Ser Asn Pro Tyr Val Met Leu Gly Ala Gly Leu
 445 450
 gta gct aaa aaa gca att gaa aaa ggc tta aaa gta cct gat tat gta 2104
 Val Ala Lys Lys Ala Ile Glu Lys Gly Leu Lys Val Pro Asp Tyr Val
 460 465 470
 aaa act tca tta gca cca ggt tca aaa gtt gtt act gga tat tta aga 2152
 Lys Thr Ser Leu Ala Pro Gly Ser Lys Val Val Thr Gly Tyr Leu Arg
 475 480 485
 gat tca ggt tta caa gaa tat ctt gat gac tta ggt ttc aac tta gtt 2200
 Asp Ser Gly Leu Gln Glu Tyr Leu Asp Asp Leu Gly Phe Asn Leu Val
 490 495 500 505
 ggt tat ggt tgt aca act tgt atc ggt aac tca ggt cca tta tta cct 2248
 Gly Tyr Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu Leu Pro
 510 515 520
 gaa att gaa aaa gca gta gct gac gaa gat tta tta gta act tct gta 2296
 Glu Ile Glu Lys Ala Val Ala Asp Glu Asp Leu Leu Val Thr Ser Val
 525 530 535
 ctt tct ggt aac cgt aac ttt gaa ggt cgt atc cat ccg tta gtt aaa 2344
 Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Ile His Pro Leu Val Lys
 540 545 550
 gct aac tac tta gct tca cca caa tta gtt gta gct tat gca tta gct 2392
 Ala Asn Tyr Leu Ala Ser Pr Gln Leu Val Val Ala Tyr Ala Leu Ala

555	560	565	
gga acg gtt gat atc gat tta cac aat gaa cct atc ggt aaa ggt aaa 2440			
Gly Thr Val Asp Ile Asp Leu His Asn Glu Pro Ile Gly Lys Gly Lys			
570	575	580	585
gat ggc gaa gat gta tac ctt aaa gat atc tgg cca agt atc aaa gaa 2488			
Asp Gly Glu Asp Val Tyr Leu Lys Asp Ile Trp Pro Ser Ile Lys Glu			
590	595	600	
gtt gca gac act gtt gat agt gtc gta acg cca gaa tta ttc tta gaa 2536			
Val Ala Asp Thr Val Asp Ser Val Val Thr Pro Glu Leu Phe Leu Glu			
605	610	615	
gaa tat gca aat gta tac gaa aat aat gaa atg tgg aat gaa atc gac 2584			
Glu Tyr Ala Asn Val Tyr Glu Asn Asn Glu Met Trp Asn Glu Ile Asp			
620	625	630	
gtt act gac gca cca tta tat gat ttc gat cca aat tca act tat att 2632			
Val Thr Asp Ala Pro Leu Tyr Asp Phe Asp Pro Asn Ser Thr Tyr Ile			
635	640	645	
caa aat cca tca ttc ttc caa ggt tta tct aaa gaa cca gga act att 2680			
Gln Asn Pro Ser Phe Phe Gln Gly Leu Ser Lys Glu Pro Gly Thr Ile			
650	655	660	665
gaa cca tta aaa gat tta cgt att atg ggt aaa ttt ggt gat tca gtt 2728			
Glu Pro Leu Lys Asp Leu Arg Ile Met Gly Lys Phe Gly Asp Ser Val			
670	675	680	
aca act gac cac att tct cca gca ggt gcg atc ggt aaa gat aca cca 2776			
Thr Thr Asp His Ile Ser Pro Ala Gly Ala Ile Gly Lys Asp Thr Pro			
685	690	695	
gca ggt aaa tat tta tta gac cat gat gtt cca att aga gaa ttt aac 2824			
Ala Gly Lys Tyr Leu Leu Asp His Asp Val Pr Ile Arg Glu Phe Asn			
700	705	710	
tct tat ggt tca aga cgt ggt aac cat gaa gta atg gta cgt ggt act 2872			

Ser Tyr Gly Ser Arg Arg Gly Asn His Glu Val Met Val Arg Gly Thr
 715 720 725
 ttc gct aat atc cgt att aaa aac caa tta gca cca ggc act gaa ggt 2920
 Phe Ala Asn Ile Arg Ile Lys Asn Gln Leu Ala Pro Gly Thr Glu Gly
 730 735 740 745
 gga ttt aca aca tat tgg cct aca gaa gaa atc atg cct atc tat gat 2968
 Gly Phe Thr Thr Tyr Trp Pro Thr Glu Glu Ile Met Pro Ile Tyr Asp
 750 755 760
 gco gct aat aca ttt gaa ttt gaa ttt ggt act ggt tta gct gtt tta gct 3016
 Ala Ala Met Arg Tyr Lys Glu Asn Gly Thr Gly Leu Ala Val Leu Ala
 765 770 775
 ggt aat gat tac ggt atg ggt tca tct cgt gac tgg gca gct aaa ggt 3064
 Gly Asn Asp Tyr Gly Met-Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly
 780 785 790
 act aac tta tta ggt gtt aaa act gtt att gca caa agt tat gaa cgt 3112
 Thr Asn Leu Leu Gly Val Lys Thr Val Ile Ala Gln Ser Tyr Glu Arg
 795 800 805
 atc cat cgt tca aac tta gta atg atg ggt gta tta cca tta caa ttt 3160
 Ile His Arg Ser Asn Leu Val Met Met Gly Val Leu Pro Leu Gln Phe
 810 815 820 825
 aaa caa ggt gag tca gct gat tct cta ggt tta gaa ggt aaa gaa gaa 3208
 Lys Gln Gly Glu Ser Ala Asp Ser Leu Gly Leu Glu Gly Lys Glu Glu
 830 835 840
 att tct gta gat atc gat gaa aat gtt aaa cca cat gat tta gta act 3256
 Ile Ser Val Asp Ile Asp Glu Asn Val Lys Pro His Asp Leu Val Thr
 845 850 855
 gtt cat gct aaa aaa gaa aac gga gaa gtt gtt gat ttt gaa gca atg 3304
 Val His Ala Lys Lys Glu Asn Gly Glu Val Val Asp Phe Glu Ala Met
 860 865 870

gtt cgt ttc gat tca tta gta gaa tta gat tat tat cgt cat ggt ggt 3352

Val Arg Phe Asp Ser Leu Val Glu Leu Asp Tyr Tyr Arg His Gly Gly

875

880

885

atc ita caa atg gta tta aga aac aaa tta gct caa taatcacaaat 3398

Ile Leu Gln Met Val Leu Arg Asn Lys Leu Ala Gln

890

895

900

gtgacttttg acagtgcataa cgtttaggtt agcactgttt ttttatgcta aactatataat 3458

gtaatgttaa tagttaagga aggattggac ttaaatgatt tatagtttga ctgaaattga 3518

accaagatai caagagacag aaaaaatggg cgigatitai catggcaati aigcaacatg 3578

gtttaagta gcgcgtacag attacattag aaaacttagga ttttagttatg ctgatatgga 3638

aaagcaaggg atcatttctc cagttacaga cttaaatatc aaatataaaa aatcaatttt 3698

ttatcctgaa aaagtaacca taaaacatg ggtggaaaaa tattcaagat tacgttctgt 3758

gtatagatat gaaattttta atgaacaggg agaacttgca actacagggtt atactgagtt 3818

aatttgtatg aaagctgata ccttttagacc aatttagatta gatcggttatt tctcagattg 3878

gcatgaaacc tatagtaaag ttgaagctt 3907

[0094]

<210> 28

<211> 901

<212> PRT

<213> *Corynebacterium thermoaminogenes*

<400> 28

Met Ala Ser Asn Phe Lys Glu Thr Ala Lys Lys Gln Phe Asp Leu Asn

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10

15

Gly Gln Ser Tyr Thr Tyr Tyr Asp Leu Lys Ser Leu Glu Glu Gln Gly

20

25

30

Leu Thr Lys Ile Ser Lys Leu Pr Tyr Ser Ile Arg Val Leu Leu Glu

35

40

45

Ser Val Leu Arg Gln Glu Asp Asp Phe Val Ile Thr Asp Asp His Ile

50	55	60
Lys Gln Leu Ala Glu Phe Gly Lys	Gly Asn Glu Gly Glu Val Pro	
65	70	75
Phe Lys Pro Ser Arg Val Ile Leu Gln Asp Phe Thr Gly Val Pro Ala		80
85	90	95
Val Val Asp Leu Ala Ser Leu Arg Lys Ala Met Asn Asp Val Gly Gly		
100	105	110
Asp Ile Asn Lys Ile Asn Pro Glu Val Pro Val Asp Leu Val Ile Asp		
115	120	125
His Ser Val Gln Val Asp Ser Tyr Ala Asn Pro Asp Ala Leu Gln Arg		
130	135	140
Asn Met Lys Leu Glu Phe Glu Arg Asn Tyr Glu Arg Tyr Gln Phe Leu		
145	150	155
Asn Trp Ala Thr Lys Ala Phe Asp Asn Tyr Asn Ala Val Pro Pro Ala		160
165	170	175
Thr Gly Ile Val His Gln Val Asn Leu Glu Tyr Leu Ala Asn Val Val		
180	185	190
His Val Arg Asp Val Asp Gly Glu Gln Thr Ala Phe Pro Asp Thr Leu		
195	200	205
Val Gly Thr Asp Ser His Thr Thr Met Ile Asn Gly Ile Gly Val Leu		
210	215	220
Gly Trp Gly Val Gly Gly Ile Glu Ala Glu Ala Gly Met Leu Gly Gln		
225	230	235
Pro Ser Tyr Phe Pro Ile Pro Glu Val Ile Gly Val Lys Leu Ser Asn		240
245	250	255
Glu Leu Pro Gln Gly Ser Thr Ala Thr Asp Leu Ala Leu Arg Val Thr		
260	265	270
Glu Glu Leu Arg Lys Arg Gly Val Val Gly Lys Phe Val Glu Phe Phe		
275	280	285

Gly Pro Gly Val Thr Asn Leu Pro Leu Ala Asp Arg Ala Thr Ile Ala
 290 295 300
 Asn Met Ala Pro Glu Tyr Gly Ala Thr Cys Gly Phe Phe Pro Val Asp
 305 310 315 320
 Glu Glu Ser Leu Lys Tyr Met Lys Leu Thr Gly Arg Lys Asp Asp His
 325 330 335
 Ile Ala Leu Val Lys Glu Tyr Leu Gln Gln Asn Asn Met Phe Phe Gln
 340 345 350
 Val Glu Asn Glu Asp Pro Glu Tyr Thr Glu Val Ile Asp Leu Asp Leu
 355 360 365
 Ser Thr Val Gln Ala Ser Leu Ser Gly Pro Lys Arg Pro Gln Asp Leu
 370 375 380
 Ile Phe Leu Ser Asp Met Lys Thr Glu Phe Glu Lys Ser Val Thr Ala
 385 390 395 400
 Pro Ala Gly Asn Gln Gly His Gly Leu Asp Glu Ser Glu Phe Asp Lys
 405 410 415
 Lys Ala Glu Ile Lys Phe Asn Asp Gly Arg Thr Ser Thr Met Lys Thr
 420 425 430
 Gly Asp Val Ala Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr Ser Asn
 435 440 445
 Pro Tyr Val Met Leu Gly Ala Gly Leu Val Ala Lys Lys Ala Ile Glu
 450 455 460
 Lys Gly Leu Lys Val Pro Asp Tyr Val Lys Thr Ser Leu Ala Pro Gly
 465 470 475 480
 Ser Lys Val Val Thr Gly Tyr Leu Arg Asp Ser Gly Leu Gln Glu Tyr
 485 490 495
 Leu Asp Asp Leu Gly Phe Asn Leu Val Gly Tyr Gly Cys Thr Thr Cys
 500 505 510
 Ile Gly Asn Ser Gly Pr Leu Leu Pr Glu Ile Glu Lys Ala Val Ala

515	520	525
Asp Glu Asp Leu Leu Val Thr Ser Val Leu Ser Gly Asn Arg Asn Phe		
530	535	540
Glu Gly Arg Ile His Pro Leu Val Lys Ala Asn Tyr Leu Ala Ser Pro		
545	550	555
Gln Leu Val Val Ala Tyr Ala Leu Ala Gly Thr Val Asp Ile Asp Leu		
565	570	575
His Asn Glu Pro Ile Gly Lys Gly Lys Asp Gly Glu Asp Val Tyr Leu		
580	585	590
Lys Asp Ile Trp Pro Ser Ile Lys Glu Val Ala Asp Thr Val Asp Ser		
595	600	605
Val Val Thr Pro Glu Leu Phe Leu Glu Glu Tyr Ala Asn Val Tyr Glu		
610	615	620
Asn Asn Glu Met Trp Asn Glu Ile Asp Val Thr Asp Ala Pro Leu Tyr		
625	630	635
Asp Phe Asp Pro Asn Ser Thr Tyr Ile Gln Asn Pro Ser Phe Phe Gln		
645	650	655
Gly Leu Ser Lys Glu Pro Gly Thr Ile Glu Pro Leu Lys Asp Leu Arg		
660	665	670
Ile Met Gly Lys Phe Gly Asp Ser Val Thr Asp His Ile Ser Pro		
675	680	685
Ala Gly Ala Ile Gly Lys Asp Thr Pro Ala Gly Lys Tyr Leu Leu Asp		
690	695	700
His Asp Val Pro Ile Arg Glu Phe Asn Ser Tyr Gly Ser Arg Arg Gly		
705	710	715
Asn His Glu Val Met Val Arg Gly Thr Phe Ala Asn Ile Arg Ile Lys		
725	730	735
Asn Gln Leu Ala Pr Gly Thr Glu Gly Gly Phe Thr Thr Tyr Trp Pr		
740	745	750

Thr Glu Glu Ile Met Pro Ile Tyr Asp Ala Ala Met Arg Tyr Lys Glu

755 760 765

Asn Gly Thr Gly Leu Ala Val Leu Ala Gly Asn Asp Tyr Gly Met Gly

770 775 780

Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr Asn Leu Leu Gly Val Lys

785 790 795 800

Thr Val Ile Ala Gln Ser Tyr Glu Arg Ile His Arg Ser Asn Leu Val

805 810 815

Met Met Gly Val Leu Pro Leu Gln Phe Lys Gln Gly Glu Ser Ala Asp

820 825 830

Ser Leu Gly Leu Glu Gly Lys Glu Glu Ile Ser Val Asp Ile Asp Glu

835 840 845

Asn Val Lys Pro His Asp Leu Val Thr Val His Ala Lys Lys Glu Asn

850 855 860

Gly Glu Val Val Asp Phe Glu Ala Met Val Arg Phe Asp Ser Leu Val

865 870 875 880

Glu Leu Asp Tyr Tyr Arg His Gly Gly Ile Leu Gln Met Val Leu Arg

885 890 895

Asn Lys Leu Ala Gln

900

【0095】

<210> 29

<211> 3006

<212> DNA

<213> *Corynebacterium thermoaminogenes*

<220>

<221> CDS

<222> (328)..(2514)

<400> 29

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 atcgccgggg agagcagcat ggtcacacgc ctgcggcgtg ccctggtgaa ggatcacggc 180
 ctggacagat cgcagggtggc attcatgggt tattggaggc agggagtggc catgaggggt 240
 tgatatcgct tccctgaggg tccgcaggcg tgcctcaccc tgtattcttgc atagttgaac 300
 aaaagagccc acataacaag gagactc atg gct aag atc atc tgg acc cgc acc 354

Met Ala Lys Ile Ile Trp Thr Arg Thr

1 5

gac gaa gca ccg ctg ctc gcg acc tac tcg ctg aag ccg gtc gtc gag 402
 Asp Glu Ala Pro Leu Leu Ala Thr Tyr Ser Leu Lys Pro Val Val Glu

10	15	20	25	
gct ttc gcc gcc acc gcg ggc atc gag gtg gag acc cgc gat atc tct				450
Ala Phe Ala Ala Thr Ala Gly Ile Glu Val Glu Thr Arg Asp Ile Ser				
30	35	40		

ctc gcc ggt cgc atc ctc gca cag ttc gcg gac cag ctc ccc gag gag 498
 Leu Ala Gly Arg Ile Leu Ala Gln Phe Ala Asp Gln Leu Pro Glu Glu

45	50	55	
cag aag gtc tcc gac gcc ctc gcc gag ctc ggc gaa ctg gct aag acc			546
Gln Lys Val Ser Asp Ala Leu Ala Glu Leu Gly Glu Leu Ala Lys Thr			

60	65	70	
ccc gaa gcc aac atc atc aag ctt ccc aac atc tcc gca tcc gta ccg			594
Pro Glu Ala Asn Ile Ile Lys Leu Pro Asn Ile Ser Ala Ser Val Pro			

75	80	85	
cag ctc aag gct gcc gta aag gaa ctg cag gaa cag ggc tac gac ctg			642
Gln Leu Lys Ala Ala Val Lys Glu Leu Gln Glu Gln Gly Tyr Asp Leu			

90	95	100	105
ccc gag tac gag gat gcc aag gac cgc tac gcc gct gtc atc ggc tcc			690

Pro Glu Tyr Glu Asp Ala Lys Asp Arg Tyr Ala Ala Val Ile Gly Ser
 110 115 120
 aac gtc aac ccg gtc ctg cgc gag ggc aac tcc gac cgc cgc gca ccg 738
 Asn Val Asn Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg Ala Pro
 125 130 135
 gtg gcc gtg aag aac ttc gtg aag aag ttc ccc cac cgc atg ggc gag 786
 Val Ala Val Lys Asn Phe Val Lys Lys Phe Pro His Arg Met Gly Glu
 140 145 150
 tgg ccc gac tcc aag acc aac gtt gcc acc atg ggt gcc gac gac 834
 Trp Ser Ala Asp Ser Lys Thr Asn Val Ala Thr Met Gly Ala Asp Asp
 155 160 165
 ttc cgc agc aat gag aag tcc gtg atc atg gac gag gcc gac acc gtg 882
 Phe Arg Ser Asn Glu Lys Ser Val Ile Met Asp Glu Ala Asp Thr Val
 170 175 180 185
 gtg atc aag cat gtc gcc gcc gac ggc acc gag acc gtg ctc aag gac 930
 Val Ile Lys His Val Ala Ala Asp Gly Thr Glu Thr Val Leu Lys Asp
 190 195 200
 agc ctc ccc ctg ctc aag ggt gag gtc atc gac ggc acc ttc atc tcc 978
 Ser Leu Pro Leu Leu Lys Gly Glu Val Ile Asp Gly Thr Phe Ile Ser
 205 210 215
 gcc aag gca ctg gac gcc ttc ctg ctc gac cag gtc aaa cgc gcc aag 1026
 Ala Lys Ala Leu Asp Ala Phe Leu Leu Asp Gln Val Lys Arg Ala Lys
 220 225 230
 gag gag ggc atc ctc ttc tcc gcc cac atg aag gcc acc atg atg aag 1074
 Glu Glu Gly Ile Leu Phe Ser Ala His Met Lys Ala Thr Met Met Lys
 235 240 245
 gtc tcc gac ccg atc atc ttc ggc cac atc gtc cgc gcc tac ttc gcc 1122
 Val Ser Asp Pr Ile Ile Phe Gly His Ile Val Arg Ala Tyr Phe Ala
 250 255 260 265

gat gtc tac gca cag tac ggt gag cag ctg ctc gcc gcc ggc ctc aac			1170
Asp Val Tyr Ala Gln Tyr Gly Glu Gln Leu Leu Ala Ala Gly Leu Asn			
270	275	280	
ggt gag aac ggt ctc gcc gcc atc tac gcc ggc ctg gac aag ctg gac			1218
Gly Glu Asn Gly Leu Ala Ala Ile Tyr Ala Gly Leu Asp Lys Leu Asp			
—	285	—	295
aac ggt gcc gag atc aag gca gcc ttc gac aag ggc ctg gaa gag ggc			1266
Asn Gly Ala Glu Ile Lys Ala Ala Phe Asp Lys Gly Leu Glu Glu Gly			
305	310		
ccc gac ctg gcc atg gtg aac tcc gcc aag ggc atc acc aac ctg cat			1314
Pro Asp Leu Ala Met Val Asn Ser Ala Lys Gly Ile Thr Asn Leu His			
315	320	325	
gtg ccc tcc gat gtc atc atc gac gcc tcc atg ccc gcc atg atc cgc			1362
Val Pro Ser Asp Val Ile Ile Asp Ala Ser Met Pro Ala Met Ile Arg			
330	335	340	345
acc tcc ggc aag atg tgg aac aag gac gac cag acc cag gat gcc ctg			1410
Thr Ser Gly Lys Met Trp Asn Lys Asp Asp Gln Thr Gln Asp Ala Leu			
350	355	360	
gct gtc atc ccg gac tcc tcc tac gcc ggt gtc tac cag acc gtc atc			1458
Ala Val Ile Pro Asp Ser Ser Tyr Ala Gly Val Tyr Gln Thr Val Ile			
365	370	375	
gag gac tgc cgc aag aat ggc gcc ttc gat ccg acc acc atg ggc acc			1506
Glu Asp Cys Arg Lys Asn Gly Ala Phe Asp Pro Thr Thr Met Gly Thr			
380	385	390	
gtc ccc aac gtc ggt ctg atg gca cag aag gcc gag gag tac ggc tcc			1554
Val Pro Asn Val Gly Leu Met Ala Gln Lys Ala Glu Glu Tyr Gly Ser			
395	400	405	
cac gac aag acc ttc cgt atc gag gcc gac ggc aag gta cag gtc gtc			1602
His Asp Lys Thr Phe Arg Ile Glu Ala Asp Gly Lys Val Gln Val Val			

410	415	420	425	
gcc tcc aac ggt gat gtc ctc atc gag cac gac gtg gag aag ggc gac				1650
Ala Ser Asn Gly Asp Val Leu Ile Glu His Asp Val Glu Lys Gly Asp				
430	435	440		
atc tgg cgc gcc tgc cag acc aag gac gcc ccg atc cag gac tgg gtc				1698
Ile Trp Arg Ala Cys Gln Thr Lys Asp Ala Pro Ile Gln Asp Trp Val				
445	450	455		
aag ctg gct gtc aac cgc gca cgt ctc tcc ggc atg ccc gct gtg ttc				1746
Lys Leu Ala Val Asn Arg Ala Arg Leu Ser Gly Met Pro Ala Val Phe				
460	465	470		
tgg ctg gat ccc gcc cgc gca cac gac cgc aac ctg acc aca ctg gtg				1794
Trp Leu Asp Pro Ala Arg Ala His Asp Arg Asn Leu Thr Thr Leu Val				
475	480	485		
gag aag tac ctg gca gac cac gac acc gag ggc ctg gac atc cag atc				1842
Glu Lys Tyr Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile Gln Ile				
490	495	500	505	
ctc tcc ccc gtc gag gcc acc cag cac gcc atc gac cgc atc cgc cgc				1890
Leu Ser Pro Val Glu Ala Thr Gln His Ala Ile Asp Arg Ile Arg Arg				
510	515	520		
ggc gag gac acc atc tcc gtc acc ggt aac gtc ctg cgt gac tac aac				1938
Gly Glu Asp Thr Ile Ser Val Thr Gly Asn Val Leu Arg Asp Tyr Asn				
525	530	535		
acc gac ctc ttc ccg atc ctc gag ctg ggc acc tcc gcc aag atg ctc				1986
Thr Asp Leu Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys Met Leu				
540	545	550		
tcc gtc gtg cca ctg atg gcc ggc ggt gga ctc ttc gag acc ggt gcc				2034
Ser Val Val Pr Leu Met Ala Gly Gly Leu Phe Glu Thr Gly Ala				
555	560	565		
ggc tcc gcc ccg aag cac gtc cag cag gtc atc gag gaa aac cac				2082

Gly Gly Ser Ala Pro Lys His Val Gln Gln Val Ile Glu Glu Asn His
 570 575 580 585
 ctg cgc tgg gat tcc ctc ggt gag ttc ctg gcc ctg gag tcc ttc 2130
 Leu Arg Trp Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe
 590 595 600
 —cgc—cac—gag—ctc—aac—acc—egc—aac—aac—acc—aag—gcc—ggt—gtc—etc—gcc 2178
 Arg His Glu Leu Asn Thr Arg Asn Asn Thr Lys Ala Gly Val Leu Ala
 605 610 615
 gat gcc ctg gac cgt egc acc gag aag ctc ctc aac gag gag aag tcc 2226
 Asp Ala Leu Asp Arg Ala Thr Glu Lys Leu Leu Asn Glu Glu Lys Ser
 620 625 630
 ccg tcc cgc aag gtc ggc gag atc gac aac cgt ggt tcc cac ttc tgg 2274
 Pro Ser Arg Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His Phe Trp
 635 640 645
 ctg gcc acc tac tgg gcc gat gaa ctg gcc aac cag acc gag gac gcc 2322
 Leu Ala Thr Tyr Trp Ala Asp Glu Leu Ala Asn Gln Thr Glu Asp Ala
 650 655 660 665
 gag ctg gct gag acc ttc gcc cct gtc gcc gag gcc ctg aac aac cag 2370
 Glu Leu Ala Glu Thr Phe Ala Pro Val Ala Glu Ala Leu Asn Asn Gln
 670 675 680
 gct gcc gac atc gac gca gca ctc atc ggt gag cag ggc aag cct gtc 2418
 Ala Ala Asp Ile Asp Ala Ala Leu Ile Gly Glu Gln Gly Lys Pro Val
 685 690 695
 gac ctg ggt ggc tac tac gca ccc tcc gat gag aag acc tcc gcg atc 2466
 Asp Leu Gly Gly Tyr Tyr Ala Pro Ser Asp Glu Lys Thr Ser Ala Ile
 700 705 710
 atg cgc ccg gtg gcc gca ttc aac gag atc atc gac tcc ctg aag aag 2514
 Met Arg Pr Val Ala Ala Phe Asn Glu Ile Ile Asp Ser Leu Lys Lys
 715 720 725

taacccttc tccggagccg acagccgacg gccacgctcc cccgcccacg ggggatcgtg 2574
 gccgtcgccc gtttctggca ctggagtgaa cacttcggtg ataatggtga gatgaacacgc 2634
 ccccggttcc ccgcacatcct gtccgcccgtt tccgcccgtgg gtctgatcgc tgccgtggc 2694
 accccccgttg ccgtcgcaga caccatcacc gcggacacccg accggaaac ctgcgtggcc 2754
 agccagaatg acaactccag cgtgatcagg ttctggatg acctggaggc cgatgtccgt 2814
 gagcagcggcc tgaccgaact ggatgcacag gacccggcc tcaagaacga catcgaggcc 2874
 ttcatcgccg aggacccgggt agcccccctcc gcagccgatc tccagagacg gctggatgca 2934
 aatgacgccc gtgagggcct ggccatgctg ctacctaatt cccgcaccga ccccgaggtg 2994
 gggaccigc ag 3006

【0096】

<210> 30

<211> 729

<212> PRT

<213> **Corynebacterium thermoaminogenes**

<400> 30

Met	Ala	Lys	Ile	Ile	Trp	Thr	Arg	Thr	Asp	Glu	Ala	Pro	Leu	Leu	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1					5					10					15
---	--	--	--	--	---	--	--	--	--	----	--	--	--	--	----

Thr	Tyr	Ser	Leu	Lys	Pro	Val	Val	Glu	Ala	Phe	Ala	Ala	Thr	Ala	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

		20				25							30		
--	--	----	--	--	--	----	--	--	--	--	--	--	----	--	--

Ile	Glu	Val	Glu	Thr	Arg	Asp	Ile	Ser	Leu	Ala	Gly	Arg	Ile	Leu	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

		35			40							45			
--	--	----	--	--	----	--	--	--	--	--	--	----	--	--	--

Gln	Phe	Ala	Asp	Gln	Leu	Pro	Glu	Glu	Gln	Lys	Val	Ser	Asp	Ala	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

		50			55					60					
--	--	----	--	--	----	--	--	--	--	----	--	--	--	--	--

Ala	Glu	Leu	Gly	Glu	Leu	Ala	Lys	Thr	Pro	Glu	Ala	Asn	Ile	Ile	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

		65			70			75					80		
--	--	----	--	--	----	--	--	----	--	--	--	--	----	--	--

Leu	Pro	Asn	Ile	Ser	Ala	Ser	Val	Pro	Gln	Leu	Lys	Ala	Ala	Val	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

			85			90						95			
--	--	--	----	--	--	----	--	--	--	--	--	----	--	--	--

Glu	Leu	Gln	Glu	Gln	Gly	Tyr	Asp	Leu	Pro	Glu	Tyr	Glu	Asp	Ala	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

100	105	110
Asp Arg Tyr Ala Ala Val Ile Gly Ser Asn Val Asn Pro Val L u Arg		
115	120	125
Glu Gly Asn Ser Asp Arg Arg Ala Pro Val Ala Val Lys Asn Phe Val		
130	135	140
Lys Lys Phe Pro His Arg Met Gly-Glu Trp Ser Ala Asp-Ser Lys Thr		
145	150	155
Asn Val Ala Thr Met Gly Ala Asp Asp Phe Arg Ser Asn Glu Lys Ser		
165	170	175
Val Ile Met Asp Glu Ala Asp Thr Val Val Ile Lys His Val Ala Ala		
180	185	190
Asp Gly Thr Glu Thr Val Leu Lys Asp Ser Leu Pro Leu Leu Lys Gly		
195	200	205
Glu Val Ile Asp Gly Thr Phe Ile Ser Ala Lys Ala Leu Asp Ala Phe		
210	215	220
Leu Leu Asp Gln Val Lys Arg Ala Lys Glu Glu Gly Ile Leu Phe Ser		
225	230	235
Ala His Met Lys Ala Thr Met Met Lys Val Ser Asp Pro Ile Ile Phe		
245	250	255
Gly His Ile Val Arg Ala Tyr Phe Ala Asp Val Tyr Ala Gln Tyr Gly		
260	265	270
Glu Gln Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn Gly Leu Ala Ala		
275	280	285
Ile Tyr Ala Gly Leu Asp Lys Leu Asp Asn Gly Ala Glu Ile Lys Ala		
290	295	300
Ala Phe Asp Lys Gly Leu Glu Glu Gly Pro Asp Leu Ala Met Val Asn		
305	310	315
Ser Ala Lys Gly Ile Thr Asn Leu His Val Pro Ser Asp Val Ile Ile		
325	330	335

Asp Ala Ser Met Pro Ala Met Ile Arg Thr Ser Gly Lys Met Trp Asn
 340 345 350
 Lys Asp Asp Gln Thr Gln Asp Ala Leu Ala Val Ile Pro Asp Ser Ser
 355 360 365
 Tyr Ala Gly Val Tyr Gln Thr Val Ile Glu Asp Cys Arg Lys Asn Gly
 370 375 380
 Ala Phe Asp Pro Thr Thr Met Gly Thr Val Pro Asn Val Gly Leu Met
 385 390 395 400
 Ala Gln Lys Ala Glu Glu Tyr Gly Ser His Asp Lys Thr Phe Arg Ile
 405 410 415
 Glu Ala Asp Gly Lys Val Gln Val Val Ala Ser Asn Gly Asp Val Leu
 420 425 430
 Ile Glu His Asp Val Glu Lys Gly Asp Ile Trp Arg Ala Cys Gln Thr
 435 440 445
 Lys Asp Ala Pro Ile Gln Asp Trp Val Lys Leu Ala Val Asn Arg Ala
 450 455 460
 Arg Leu Ser Gly Met Pro Ala Val Phe Trp Leu Asp Pro Ala Arg Ala
 465 470 475 480
 His Asp Arg Asn Leu Thr Thr Leu Val Glu Lys Tyr Leu Ala Asp His
 485 490 495
 Asp Thr Glu Gly Leu Asp Ile Gln Ile Leu Ser Pro Val Glu Ala Thr
 500 505 510
 Gln His Ala Ile Asp Arg Ile Arg Arg Gly Glu Asp Thr Ile Ser Val
 515 520 525
 Thr Gly Asn Val Leu Arg Asp Tyr Asn Thr Asp Leu Phe Pro Ile Leu
 530 535 540
 Glu Leu Gly Thr Ser Ala Lys Met Leu Ser Val Val Pr Leu Met Ala
 545 550 555 560
 Gly Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser Ala Pr Lys His

565	570	575
Val Gln Gln Val Ile Glu Glu Asn His Leu Arg Trp Asp Ser Leu Gly		
580	585	590
Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu Leu Asn Thr Arg		
595	600	605
Asn Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu Asp Arg Ala Thr		
610	615	620
Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg Lys Val Gly Glu		
625	630	635
Ile Asp Asn Arg Gly Ser His Phe Trp Leu Ala Thr Tyr Trp Ala Asp		
645	650	655
Glu Leu Ala Asn Gln Thr Glu Asp Ala Glu Leu Ala Glu Thr Phe Ala		
660	665	670
Pro Val Ala Glu Ala Leu Asn Asn Gln Ala Ala Asp Ile Asp Ala Ala		
675	680	685
Leu Ile Gly Glu Gln Gly Lys Pro Val Asp Leu Gly Gly Tyr Tyr Ala		
690	695	700
Pro Ser Asp Glu Lys Thr Ser Ala Ile Met Arg Pro Val Ala Ala Phe		
705	710	715
Asn Glu Ile Ile Asp Ser Leu Lys Lys		
725		

【0097】

- <210> 31
- <211> 2322
- <212> DNA
- <213> **Corynebacterium thermoaminogenes**

<220>

<221> CDS

<222> (806)..(2212)

<400> 31

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 tcataacgtc cttatgaatt tcgcagttat tagttattta aatagagaat caaactccga 120
 cctaggctct-gccgatgcta-aaagtca-gtgcacccttgg-ggcgccttcat-ttgaaactgc 180
 gaccaagctc atgaatgcgc gaaagcattt ccattataag ggtaagctgt aagaatagt 240
 ggagaaaaatg ttcaagtcgtg ttcttaactca cttgagaaat tccatTTTC tggccttc 300
 tcaaaatagai taagigggccc gtaatgcigga ttictagaat atttagaagc gcgcacaactc 360
 atgattatgt attgtataag cctcaaagac cgaatagatt actaacatTTT aagtggacca 420
 gagcgttaga agctttgttag agtgctcatt cttgctgac ggcaagggtt tcctaccatg 480
 agatagatcg gcagatagtt ggtttgtaaa aatTTTAAG gacggtccgc aatgtcaatt 540
 cttaacaga tcatTTCTT catcaacacc atcttgggtt atggtctgca cgctggttct 600
 tccgcTTCCA gcaacCTTC tcacacgatc ggcctgttct aggccataatt ggtataagg 660
 ctgtgtaca gtcggccgcg tgattgtgc ttttaggcg cccgcgcggg cgattttcgg 720
 tttcatctt tttaaattg agtttggaaag atcaagtgcc cccggatgca cgacaatgct 780
 atgcccgaaca cgtattgttg aaatc gtg act gaa cat tat gac gta gta gta 832

Val Thr Glu His Tyr Asp Val Val Val

1 5

ctc gga gct ggc ccc ggt ggc tat gtc tcc gcc atc cgc gcc gcg cag 880

Leu Gly Ala Gly Pro Gly Gly Tyr Val Ser Ala Ile Arg Ala Ala Gln

10 15 20 25

ctc ggt aag aaa gtt gcg gtt atc gag aag cag tac tgg gga ggt gtc 928

Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr Trp Gly Gly Val

30 35 40

tgc ctg aat gtg ggt tgt atc cca tct aag gcg ttg atc aag aac gct 976

Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Ala Leu Ile Lys Asn Ala

45 50 55

gag atc gcc cac atc ttc aac cat gag aag aag acc ttc ggc atc aac 1024

Glu Ile Ala His Ile Phe Asn His Glu Lys Lys Thr Phe Gly Ile Asn
 60 65 70
 ggc gag gtc acc ttc aac tac gag gat gcc cac aag cgt tcc cgt ggt 1072
 Gly Glu Val Thr Phe Asn Tyr Glu Asp Ala His Lys Arg Ser Arg Gly
 75 80 85
 gtc tcc gac aag atc gtc ggc ggt gtt cac tac ttg atg aag aag aac 1120
 Val Ser Asp Lys Ile Val Gly Gly Val His Tyr Leu Met Lys Lys Asn
 90 95 100 105
 aag atc acc gag atc gac ggt ttc ggc acc ttc aag gat gcc aag acc 1168
 Lys Ile Thr Glu Ile Asp Gly Phe Gly Thr Phe Lys Asp Ala Lys Thr
 110 115 120
 atc gag gtg acc gat ggt aag gat gcc ggc aag acc gtc acc ttc gat 1216
 Ile Glu Val Thr Asp Gly Lys Asp Ala Gly Lys Thr Val Thr Phe Asp
 125 130 135
 gac tgc atc atc gcc acc ggt tcc gtg gtc aac tcc ctc cgt ggt gtt 1264
 Asp Cys Ile Ile Ala Thr Gly Ser Val Val Asn Ser Leu Arg Gly Val
 140 145 150
 gag ttc tcc gag aac gtg gtc tcc tac gag gag cag atc ctc aac ccg 1312
 Glu Phe Ser Glu Asn Val Val Ser Tyr Glu Glu Gln Ile Leu Asn Pro
 155 160 165
 gtg gcg cct aag aag atg gtc atc gtc ggt ggc ggc gcc atc ggt atg 1360
 Val Ala Pro Lys Lys Met Val Ile Val Gly Gly Ala Ile Gly Met
 170 175 180 185
 gaa ttc gcc tac gtt ctg ggc aac tac ggt gtg gac gta acc ctc atc 1408
 Glu Phe Ala Tyr Val Leu Gly Asn Tyr Gly Val Asp Val Thr Leu Ile
 190 195 200
 gag ttc atg gac cgc gtt ctg ccg aac gag gat cca gag gtg tcc aag 1456
 Glu Phe Met Asp Arg Val Leu Pro Asn Glu Asp Pro Glu Val Ser Lys
 205 210 215

gtt atc gcc aag gcc tac aag aag atg ggc atc aag ctc ctc ccg ggc		1504	
Val Ile Ala Lys Ala Tyr Lys Lys Met Gly Ile Lys L u Leu Pro Gly			
220	225	230	
cac gca acc acc gcg gtg cgc gac aat ggc gat tcc gtt gag gtc gat		1552	
His Ala Thr Thr Ala Val Arg Asp Asn Gly Asp Ser Val Glu Val Asp			
235	240	245	
tac cag aag aag ggc tcg gac aag acc gag acc atc acc gtc gac cgt		1600	
Tyr Gln Lys Lys Gly Ser Asp Lys Thr Glu Thr Ile Thr Val Asp Arg			
250	255	260	265
gtt ctt atc tcc gtc ggc ttc cgc cca cgc gtc gag ggc ttc ggc ctg		1648	
Val Leu Ile Ser Val Gly Phe Arg Pro Arg Val Glu Gly Phe Gly Leu			
270	275	280	
gag aac acc ggc gtc aag ctc acc gaa cgc ggt gcc atc gac att gat		1696	
Glu Asn Thr Gly Val Lys Leu Thr Glu Arg Gly Ala Ile Asp Ile Asp			
285	290	295	
gag cat atg cgc acc aac gtc gac ggc atc tac gcc atc ggt gac gtc		1744	
Glu His Met Arg Thr Asn Val Asp Gly Ile Tyr Ala Ile Gly Asp Val			
300	305	310	
acc gcc aag ctg cag ctg gca cac gtc gcc gag gca cag ggc att gtc		1792	
Thr Ala Lys Leu Gln Leu Ala His Val Ala Glu Ala Gln Gly Ile Val			
315	320	325	
gcc gcc gag aca ctc gcc ggc gca gaa acc cag acc ctg ggc gac tac		1840	
Ala Ala Glu Thr Leu Ala Gly Ala Glu Thr Gln Thr Leu Gly Asp Tyr			
330	335	340	345
atg atg atg ccg cgt gcc acc ttc tgc aac cca cag gtt gcc tcc ttc		1888	
Met Met Met Pro Arg Ala Thr Phe Cys Asn Pro Gln Val Ala Ser Phe			
350	355	360	
ggt tac acc gag gag cag gcc aag gag aag tgg ccg gat cga gag atc		1936	
Gly Tyr Thr Glu Glu Gln Ala Lys Glu Lys Trp Pro Asp Arg Glu Ile			

365

370

375

aag gtg tcc tcc ttc ccg ttc tcc gcg aac ggc aag gcc gtc ggc ctg 1984

Lys Val Ser Ser Phe Pro Phe Ser Ala Asn Gly Lys Ala Val Gly Leu

380

385

390

gct gag acc gat ggt ttc gcc aag atc gtc gcc gac gct gag ttc ggt 2032

Ala Glu Thr Asp Gly Phe Ala Lys Ile Val Ala Asp Ala Glu Phe Gly

395

400

405

gaa ctg ctg ggt ggc cac att gtc ggt gcc aac gcc tcc gag ctg ctc 2080

Glu Leu Leu Gly Gly His Ile Val Gly Ala Asn Ala Ser Glu Leu Leu

410 415 420 425

aac gag ctg gtg ctg gcc cag aac tgg gat ctc acc acc gag gag atc 2128

Asn Glu Leu Val Leu Ala Gln Asn Trp Asp Leu Thr Thr Glu Glu Ile

430 435 440

agc cgc agc gtc cac atc cac ccg acc ctg tcg gag gct gtc aag gaa 2176

Ser Arg Ser Val His Ile His Pro Thr Leu Ser Glu Ala Val Lys Glu

445 450 455

gct gcc cac ggc gtc aac ggc cac atg atc aac ttc taaatcccgt 2222

Ala Ala His Gly Val Asn Gly His Met Ile Asn Phe

460 465

cagacaaaatg caaatccccct caccgatggc atatcggtga ggggattttc tcatgcacgt 2282

aaaatataa tccatggcaa ggaaagtgcga caacagcgcc 2322

[0098]

<210> 32

<211> 469

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 32

Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly

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Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val			
20	25	30	
Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile			
35	40	45	
Pro Ser Lys Ala Leu Ile Lys Asn Ala Glu Ile Ala His Ile Phe Asn			
50	55	60	
His Glu Lys Lys Thr Phe Gly Ile Asn Gly Glu Val Thr Phe Asn Tyr			
65	70	75	80
Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser Asp Lys Ile Val Gly			
85	90	95	
Gly Val His Tyr Leu Met Lys Asn Lys Ile Thr Glu Ile Asp Gly			
100	105	110	
Phe Gly Thr Phe Lys Asp Ala Lys Thr Ile Glu Val Thr Asp Gly Lys			
115	120	125	
Asp Ala Gly Lys Thr Val Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly			
130	135	140	
Ser Val Val Asn Ser Leu Arg Gly Val Glu Phe Ser Glu Asn Val Val			
145	150	155	160
Ser Tyr Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val			
165	170	175	
Ile Val Gly Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly			
180	185	190	
Asn Tyr Gly Val Asp Val Thr Leu Ile Glu Phe Met Asp Arg Val Leu			
195	200	205	
Pro Asn Glu Asp Pr Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys			
210	215	220	
Lys Met Gly Ile Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg			
225	230	235	240

Asp Asn Gly Asp Ser Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp
 245 250 255
 Lys Thr Glu Thr Ile Thr Val Asp Arg Val Leu Ile Ser Val Gly Phe
 260 265 270
 Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu
 275 280 285
 Thr Glu Arg Gly Ala Ile Asp Ile Asp Glu His Met Arg Thr Asn Val
 290 295 300
 Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala
 305 310 315 320
 His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Leu Ala Gly
 325 330 335
 Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr
 340 345 350
 Phe Cys Asn Pro Gln Val Ala Ser Phe Gly Tyr Thr Glu Glu Gln Ala
 355 360 365
 Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ser Ser Phe Pro Phe
 370 375 380
 Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala
 385 390 395 400
 Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu Leu Gly His Ile
 405 410 415
 Val Gly Ala Asn Ala Ser Glu Leu Leu Asn Glu Leu Val Leu Ala Gln
 420 425 430
 Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His
 435 440 445
 Pr Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Val Asn Gly
 450 455 460
 His Met Ile Asn Phe

465

[0099]

<210> 33

<211> 4096

<212> DNA

<213> *Corynebacterium thermoaminogenes*

<220>

<221> 1 000

<222> (250), (3951)

<400> 33

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gggagcgaat ggaacctacg caacaatgtg gcatttagta ggttgacagg atattttagg 120
aaagacttgt taccaaaagg tgctaatact ggggtgctag gtccccgcga ccggaaccag 180
cgttacagtg gataaaataa agcccattha gaaccctcaa caagcaagga aaagaggcga 240
gtacctgccc gtg agc agc gct agt act ttc ggc cag aac gcg tgg ctg gtg 291

Val Ser Ser Ala Ser Thr Phe Gly Gln Asn Ala Trp Leu Val

1 5 10

gat gag atg ttc cag cag ttc aag aag gac ccc cag tcc gtg gac aag 339

Asp Glu Met Phe Gln Gln Phe Lys Lys Asp Pro Gln Ser Val Asp Lys

15 **20** **25** **-** **30**

gaa tgg aga gag ctc ttc gag tct cag ggg ggt ccc cag gct gaa aag 387

Glu Trp Arg Glu Leu Phe Glu Ser Gln Gly Gly Pro Gln Ala Glu Lys

35 40 45

gct acc ccc gcc acc ccc gaa gcc aag aag gca gct tcg tcg cag tcc 435

Ala Thr Pro Ala Thr Pr Glu Ala Lys Lys Ala Ala Ser Ser Gln Ser

50 55 60

tca act tcc gga cag tcc acc gcc aag gct gcc cct gcc gcc aag acc 483

Ser Thr Ser Gly Gln Ser Thr Ala Lys Ala Ala Pro Ala Ala Lys Thr

65

70

75

gca ccg gcc tct gcg cca gcc aag gct gcc cct gtt aag caa aac cag 531

Ala Pro Ala Ser Ala Pro Ala Lys Ala Ala Pro Val Lys Gln Asn Gln

80

85

90

gcg tcc aag cct gcc aag aag gcc aag gag tcc ccc ctg tcc aag cca 579

Ala Ser Lys Pro Ala Lys Lys Ala Lys Glu Ser Pro Leu Ser Lys Pro

95

100

105

110

gct gcc atg cct gag tgg gga aac acc tcc ttc agg ggc atc ttc aag 627

Ala Ala Met Pro Glu Pro Gly Thr Thr Pro Leu Arg Gly Ile Phe Lys

115

120

125

tcc atc gcc aag aac atg gac ctc tcc ctc gag gtg ccc acc gcc acc 675

Ser Ile Ala Lys Asn Met Asp Leu Ser Leu Glu Val Pro Thr Ala Thr

130

135

140

tcc gtc cgc gac atg ccc gcg cgc ctc atg ttc gag aac cgc gcc atg 723

Ser Val Arg Asp Met Pro Ala Arg Leu Met Phe Glu Asn Arg Ala Met

145

150

155

gtc aac gac cag ctc aag cgc acc cgt ggc ggc aag atc tcc ttc acc 771

Val Asn Asp Gln Leu Lys Arg Thr Arg Gly Gly Lys Ile Ser Phe Thr

160

165

170

cac atc atc ggc tac gcc atg gtg aag gct gtc atg gca cac ccc gac 819

His Ile Ile Gly Tyr Ala Met Val Lys Ala Val Met Ala His Pro Asp

175

180

185

190

atg aac aac tcc tat gac atc gtc gac ggc aag ccg tcc ctg gtc gtc 867

Met Asn Asn Ser Tyr Asp Ile Val Asp Gly Lys Pro Ser Leu Val Val

195

200

205

ccg gag cac atc aac ctc ggc ctg gcc atc gac ctc ccc cag aag gac 915

Pro Glu His Ile Asn Leu Gly L u Ala Ile Asp L u Pr Gln Lys Asp

210

215

220

ggc tcc cgt gcc ctc gtg gtc gcc gcc atc aag gaa acc gag aag atg 963
 Gly Ser Arg Ala Leu Val Val Ala Ala Ile Lys Glu Thr Glu Lys Met
 225 230 235
 acc ttc tcc cag ttc ctg gag gcc tat gag gac gtt gtg gca cgc tcc 1011
 Thr Phe Ser Gln Phe Leu Glu Ala Tyr Glu Asp Val Val Ala Arg Ser
 240 245 250
 cgc gtc ggc aag ctc acc atg gat gac tac cag ggt gtc acc atc tcc 1059
 Arg Val Gly Lys Leu Thr Met Asp Asp Tyr Gln Gly Val Thr Ile Ser
 255 260 265 270
 ttg acc aac ccg ggt ggc atc ggt acc cgc cac tcc atc ccg cgt ctg 1107
 Leu Thr Asn Pro Gly Gly Ile Gly Thr Arg His Ser Ile Pro Arg Leu
 275 280 285
 acc aag ggc cag ggc acc atc atc ggt gtc ggt tcc atg gac tac ccg 1155
 Thr Lys Gly Gln Gly Thr Ile Ile Gly Val Gly Ser Met Asp Tyr Pro
 290 295 300
 gcc gag ttc cag ggt gcc tcc gag gac cgt ctc gcc gag ctc ggt gtg 1203
 Ala Glu Phe Gln Gly Ala Ser Glu Asp Arg Leu Ala Glu Leu Gly Val
 305 310 315
 ggc aag ctc gtc acc atc acc tcc acc tac gat cac cgc gtc atc cag 1251
 Gly Lys Leu Val Thr Ile Thr Ser Thr Tyr Asp His Arg Val Ile Gln
 320 325 330
 ggc gcg gaa tcc ggt gag ttc ctg cgc acc atg tcc cag ctg ctc gtg 1299
 Gly Ala Glu Ser Gly Glu Phe Leu Arg Thr Met Ser Gln Leu Leu Val
 335 340 345 350
 gac gat gcg ttc tgg gat cac atc ttc gag gag atg aac gtt ccc tac 1347
 Asp Asp Ala Phe Trp Asp His Ile Phe Glu Glu Met Asn Val Pr Tyr
 355 360 365
 acc ccg atg cgc tgg gca cag gac ctg ccc aac acc ggt gtg gac aag 1395
 Thr Pr Met Arg Trp Ala Gln Asp Leu Pro Asn Thr Gly Val Asp Lys

370	375	380	
aac acc cgt gtc atg cag ctc atc gag gcc tac cgc tcc cgc ggt cac			1443
Asn Thr Arg Val Met Gln Leu Ile Glu Ala Tyr Arg Ser Arg Gly His			
385	390	395	
ctc atc gcc gac acc aac cca ctg ccc tgg gtc cag ccc ggc atg ccc			1491
-Leu-Ile-Ala-Asp-Thr-Asn-Pro-Leu-Pro-Trp Val Gln Pro Gly Met Pro			
400	405	410	
gtc ccg gat cac cgt gac ctc gac atc gag acc cac ggc ctg acc ctg			1539
Val Pro Asp His Arg Asp Leu Asp Ile Glu Thr His Gly Leu Thr Leu			
415	420	425	430
tgg gat ctg gac cgt acc ttc cac gtc ggt ggt ttc ggt ggc aag gag			1587
Trp Asp Leu Asp Arg Thr Phe His Val Gly Gly Phe Gly Lys Glu			
435	440	445	
acc atg acc ctg cgc gag gtg ctc agc cgc ctc cgc gcc gcc tac acc			1635
Thr Met Thr Leu Arg Glu Val Leu Ser Arg Leu Arg Ala Ala Tyr Thr			
450	455	460	
ctc aag gtc ggc tcc gag tac acc cac atc ctc gac cgc gat gag cgc			1683
Leu Lys Val Gly Ser Glu Tyr Thr His Ile Leu Asp Arg Asp Glu Arg			
465	470	475	
acc tgg ctg cag gac cgc ctc gag gcc ggt atg ccc aag ccc acc gcc			1731
Thr Trp Leu Gln Asp Arg Leu Glu Ala Gly Met Pro Lys Pro Thr Ala			
480	485	490	
gcc gag cag aag tac atc ctg cag aag ctc aac gcc gcc gag gca ttc			1779
Ala Glu Gln Lys Tyr Ile Leu Gln Lys Leu Asn Ala Ala Glu Ala Phe			
495	500	505	510
gag aac ttc ctg cag acc aag tac gtc ggc cag aag cgt ttc tcc ctc			1827
Glu Asn Phe Leu Gln Thr Lys Tyr Val Gly Gln Lys Arg Phe Ser Leu			
515	520	525	
gag ggt gcc gag tca ctg atc ccg ctg atg gac tcc gcc atc gac acc			1875

Glu Gly Ala Glu Ser Leu Ile Pro Leu Met Asp Ser Ala Ile Asp Thr

530 535 540

gcc gca ggc cag ggc ctt gac gag gtc gtc atc ggc atg ccc cac cgt 1923
Ala Ala Gly Gln Gly Leu Asp Glu Val Val Ile Gly Met Pro His Arg

545 550 555

ggt cgc ctc aac gtg ctg ttc aac atc gtc ggc aag cca ctg gcc tcg 1971

Gly Arg Leu Asn Val Leu Phe Asn Ile Val Gly Lys Pro Leu Ala Ser

560 565 570

atc ttc aac gag ttc gag ggc cag atg gag cag ggc cag atc ggt ggc 2019

Ile Phe Asn Glu Phe Glu Gly Gln Met Glu Gln Gly Gln Ile Gly Gly

575 580 585 590

tcc ggt gac gtg aag tac cac ctc ggt tcc gag ggc acc cac ctg cag 2067

Ser Gly Asp Val Lys Tyr His Leu Gly Ser Glu Gly Thr His Leu Gln

595 600 605

atg ttc ggc gac ggc gag atc aag gtc tcc ctc acc gcc aac ccc tcc 2115

Met Phe Gly Asp Gly Glu Ile Lys Val Ser Leu Thr Ala Asn Pro Ser

610 615 620

cac ctc gag gcc gtc aac ccg gtc gtg gag ggc atc gtc cgc gcc aag 2163

His Leu Glu Ala Val Asn Pro Val Val Glu Gly Ile Val Arg Ala Lys

625 630 635

cag gac atc ctg gac aag ggc ccg gac ggc tac acc gtc gtc ccg ctg 2211

Gln Asp Ile Leu Asp Lys Gly Pro Asp Gly Tyr Thr Val Val Pro Leu

640 645 650

ctg ctc cac ggt gac gcc gcc ttc gcc ggc ctg ggc atc gtg ccc gag 2259

Leu Leu His Gly Asp Ala Ala Phe Ala Gly Leu Gly Ile Val Pro Glu

655 660 665 670

acc atc aac ctc gca gcc ctg cgt ggt tac gat gtc ggt ggc acc atc 2307

Thr Ile Asn Leu Ala Ala Leu Arg Gly Tyr Asp Val Gly Gly Thr Ile

675 680 685

cac atc gtg gtc aac aac cag atc ggc ttc acc acc acc ccg gac tcc 2355
 His Ile Val Val Asn Asn Gln Ile Gly Phe Thr Thr Pro Asp Ser
 690 695 700
 agc cgt tcc atg cac tac gcc acc gac tgc gcc aag gcc ttc ggt tgc 2403
 Ser Arg Ser Met His Tyr Ala Thr Asp Cys Ala Lys Ala Phe Gly Cys
 705 710 715
 ccg gtg ttc cac gtc aac ggt gac gac ccc gag gct gtg gtc tgg gtc 2451
 Pro Val Phe His Val Asn Gly Asp Asp Pro Glu Ala Val Val Trp Val
 720 725 730
 ggc cag ctg gcc acc gag tac cgt cgc cgc ttc ggc aag gat gtc ttc 2499
 Gly Gln Leu Ala Thr Glu Tyr Arg Arg Arg Phe Gly Lys Asp Val Phe
 735 740 745 750
 atc gac ctc atc tgc tac cgc ctg cgc ggc cac aac gag gct gat gac 2547
 Ile Asp Leu Ile Cys Tyr Arg Leu Arg Gly His Asn Glu Ala Asp Asp
 755 760 765
 cca tcc atg acc cag ccg aag atg tac gag ctg atc acc ggc cgc gac 2595
 Pro Ser Met Thr Gln Pro Lys Met Tyr Glu Leu Ile Thr Gly Arg Asp
 770 775 780
 tcc gtg cgt gcc acc tac acc gag gac ctc ctc ggc cgt ggt gac ctc 2643
 Ser Val Arg Ala Thr Tyr Thr Glu Asp Leu Leu Gly Arg Gly Asp Leu
 785 790 795
 tcc ccc gag gac gcc gag gcc gtt gtc cgc gac ttc cac gac cag atg 2691
 Ser Pro Glu Asp Ala Glu Ala Val Val Arg Asp Phe His Asp Gln Met
 800 805 810
 gaa-tcc gtg ttc aac gag gtc aag gaa gcc ggc aag aag cag cct gat 2739
 Glu Ser Val Phe Asn Glu Val Lys Glu Ala Gly Lys Lys Gln Pro Asp
 815 820 825 830
 gag cag acc ggc atc acc ggt tcc cag gaa ctg acc cgt ggc ctg gac 2787
 Glu Gln Thr Gly Ile Thr Gly Ser Gln Glu Leu Thr Arg Gly Leu Asp

835	840	845	
acc aac atc acc cgc gag gaa ctg gtc gaa ctc ggc cag gcc ttc gtc			2835
Thr Asn Ile Thr Arg Glu Glu Leu Val Glu Leu Gly Gln Ala Phe Val			
850	855	860	.
aac acc cca gag ggc ttc acc tac cac cca cgt gtg gca ccg gtg gcc			2883
Asn Thr Pro Glu Gly Phe Thr Tyr His Pro Arg Val Ala Pro Val Ala			
865	870	875	
aag aag cgt gcc gag tcc gtc acc gag ggt ggc atc gac tgg gca tgg			2931
Lys Lys Arg Ala Glu Ser Val Thr Glu Gly Gly Ile Asp Trp Ala Trp			
880	885	890	
ggc gag ctc atc gcc ttc ggc tcc ctg gcc acc tcc ggc agg ctg gtc			2979
Gly Glu Leu Ile Ala Phe Gly Ser Leu Ala Thr Ser Gly Arg Leu Val			
895	900	905	910
cgc ctc gcc ggt gag gat tcc cgc cgt ggt acc ttc acc cag cgt cac			3027
Arg Leu Ala Gly Glu Asp Ser Arg Arg Gly Thr Phe Thr Gln Arg His			
915	920	925	
gcc gtg gcc atc gac ccg aac acc gcc gag gag ttc aac ccg ctc cac			3075
Ala Val Ala Ile Asp Pro Asn Thr Ala Glu Glu Phe Asn Pro Leu His			
930	935	940	
gag ctg gca cag gcc aag ggc ggc aag ttc ctc gtc tac aac tcc			3123
Glu Leu Ala Gln Ala Lys Gly Gly Lys Phe Leu Val Tyr Asn Ser			
945	950	955	
gcg ctg acc gag tac gcg ggt atg ggc ttc gaa tac ggc tac tcc gtg			3171
Ala Leu Thr Glu Tyr Ala Gly Met Gly Phe Glu Tyr Gly Tyr Ser Val			
960	965	970	
ggc aac ccg gac gcc gtg gtg tcc tgg gag gca cag ttc ggt gac ttc			3219
Gly Asn Pr Asp Ala Val Val Ser Trp Glu Ala Gln Phe Gly Asp Phe			
975	980	985	990
gcc aac ggt gca cag acc atc atc gat gag tac atc tcc tcc ggt gag			3267

Ala Asn Gly Ala Gln Thr Ile Ile Asp Glu Tyr Ile Ser Ser Gly Glu
 995 1000 1005
 gcc aag tgg ggc cag acc tcc tcg gtc atc ctg ctg ctg ccc cac ggt 3315
 Ala Lys Trp Gly Gln Thr Ser Ser Val Ile Leu Leu Leu Pro His Gly
 1010 1015 1020
 tac gag ggc cag ggt ccg gac cac tcc tcc gca cgc atc gag cgt ttc 3363
 Tyr Glu Gly Gln Gly Pro Asp His Ser Ser Ala Arg Ile Glu Arg Phe
 1025 1030 1035
 ctg cag ctg tgc gcc gag ggt tcc atg acc atc gcc cag ccg acc acc 3411
 Leu Gln Leu Cys Ala Glu Gly Ser Met Thr Ile Ala Gln Pro Thr Thr
 1040 1045 1050
 ccg gcg aac tac ttc cac ctg ctg cgt cgt cac gca ctg ggc aag atg 3459
 Pro Ala Asn Tyr Phe His Leu Leu Arg Arg His Ala Leu Gly Lys Met
 1055 1060 1065 1070
 aag cgcc ccg ctg gtc gtc ttc acc ccg aag tcc atg ctg cgc aac aag 3507
 Lys Arg Pro Leu Val Val Phe Thr Pro Lys Ser Met Leu Arg Asn Lys
 1075 1080 1085
 gcc gcc acc tcc gct ccg gag gag ttc acc gag gtc acc cgc ttc aag 3555
 Ala Ala Thr Ser Ala Pro Glu Glu Phe Thr Glu Val Thr Arg Phe Lys
 1090 1095 1100
 tcc gtg atc gac gat ccg aac gtg gcg gat gcc tcc aag gtg aag aag 3603
 Ser Val Ile Asp Asp Pro Asn Val Ala Asp Ala Ser Lys Val Lys Lys
 1105 1110 1115
 atc atg ctg tgc tcc ggc aag atc tac tac gaa ctg gcc aag cgc aag 3651
 Ile Met Leu Cys Ser Gly Lys Ile Tyr Tyr Glu Leu Ala Lys Arg Lys
 1120 1125 1130
 gag aag gac aac cgc gac gac atc gcg atc gtg cgc atc gag atg ctg 3699
 Glu Lys Asp Asn Arg Asp Asp Ile Ala Ile Val Arg Ile Glu Met Leu
 1135 1140 1145 1150

cac ccg atc ccg ttc aac cgt ctg cgc gac gcc ttc gac ggc tac ccc 3747
 His Pro Ile Pro Phe Asn Arg Leu Arg Asp Ala Phe Asp Gly Tyr Pro
 1155 1160 1165
 aac gcc gag gag atc ctg ttc gtt cag gag ccg gca aac cag ggt 3795
 Asn Ala Glu Glu Ile Leu Phe Val Gln Asp Glu Pro Ala Asn Gln Gly
 1170 1175 1180
 gcc tgg ccg ttc tac cag gag cac ctg ccc aac ctc atc gag ggc atg 3843
 Ala Trp Pro Phe Tyr Gln Glu His Leu Pro Asn Leu Ile Glu Gly Met
 1185 1190 1195
 ctc ccg atg cgt cgc atc tcg cgc cgt tcc cag tcc tcg act gcg acc 3891
 Leu Pro Met Arg Arg Ile Ser Arg Arg Ser Gln Ser Ser Thr Ala Thr
 1200 1205 1210
 ggt atc gcg aag gtg cac acc atc gag cag cag aag ctg ctg gat gat 3939
 Gly Ile Ala Lys Val His Thr Ile Glu Gln Gln Lys Leu Leu Asp Asp
 1215 1220 1225 1230
 gcg ttc aac gca taaacgttaa tacagcggtt gataccttga accccgcccgc 3991
 Ala Phe Asn Ala
 accctttaga tgccggcggtt gtttgcttt gcctgcatacg gcgataatat tcatacac 4051
 ccatcacgtt taagttctgc atttggatcg tgcgagcatttccgg 4096
 【0100】
 <210> 34
 <211> 1234
 <212> PRT
 <213> Corynebacterium thermoaminogenes
 <400> 34
 Val Ser Ser Ala Ser Thr Phe Gly Gln Asn Ala Trp Leu Val Asp Glu
 1 5 10 15
 Met Phe Gln Gln Phe Lys Lys Asp Pro Gln Ser Val Asp Lys Glu Trp

20	25	30
Arg Glu Leu Phe Glu Ser Gln Gly Gly Pro Gln Ala Glu Lys Ala Thr		
35	40	45
Pro Ala Thr Pro Glu Ala Lys Lys Ala Ala Ser Ser Gln Ser Ser Thr		
50	55	60
Ser Gly Gln Ser Thr Ala Lys Ala Ala Pro Ala Ala Lys Thr Ala Pro		
65	70	75
Ala Ser Ala Pro Ala Lys Ala Ala Pro Val Lys Gln Asn Gln Ala Ser		
85	90	95
Lys Pro Ala Lys Lys Ala Lys Glu Ser Pro Leu Ser Lys Pro Ala Ala		
100	105	110
Met Pro Glu Pro Gly Thr Thr Pro Leu Arg Gly Ile Phe Lys Ser Ile		
115	120	125
Ala Lys Asn Met Asp Leu Ser Leu Glu Val Pro Thr Ala Thr Ser Val		
130	135	140
Arg Asp Met Pro Ala Arg Leu Met Phe Glu Asn Arg Ala Met Val Asn		
145	150	155
Asp Gln Leu Lys Arg Thr Arg Gly Gly Lys Ile Ser Phe Thr His Ile		
165	170	175
Ile Gly Tyr Ala Met Val Lys Ala Val Met Ala His Pro Asp Met Asn		
180	185	190
Asn Ser Tyr Asp Ile Val Asp Gly Lys Pro Ser Leu Val Val Pro Glu		
195	200	205
His Ile Asn Leu Gly Leu Ala Ile Asp Leu Pro Gln Lys Asp Gly Ser		
210	215	220
Arg Ala Leu Val Val Ala Ala Ile Lys Glu Thr Glu Lys Met Thr Phe		
225	230	235
Ser Gln Phe Leu Glu Ala Tyr Glu Asp Val Val Ala Arg Ser Arg Val		
245	250	255

Gly Lys Leu Thr Met Asp Asp Tyr Gln Gly Val Thr Ile Ser Leu Thr
 260 265 270

Asn Pro Gly Gly Ile Gly Thr Arg His Ser Ile Pro Arg Leu Thr Lys
 275 280 285

Gly Gln Gly Thr Ile Ile Gly Val Gly Ser Met Asp Tyr Pro Ala Glu
 290 295 300

Phe Gln Gly Ala Ser Glu Asp Arg Leu Ala Glu Leu Gly Val Gly Lys
 305 310 315 320

Leu Val Phe Thr Ser Thr Tyr Asp His Arg Val Ala Glu Ala
 325 330 335

Glu Ser Gly Glu Phe Leu Arg Thr Met Ser Gln Leu Leu Val Asp Asp
 340 345 350

Ala Phe Trp Asp His Ile Phe Glu Glu Met Asn Val Pro Tyr Thr Pro
 355 360 365

Met Arg Trp Ala Gln Asp Leu Pro Asn Thr Gly Val Asp Lys Asn Thr
 370 375 380

Arg Val Met Gln Leu Ile Glu Ala Tyr Arg Ser Arg Gly His Leu Ile
 385 390 395 400

Ala Asp Thr Asn Pro Leu Pro Trp Val Gln Pro Gly Met Pro Val Pro
 405 410 415

Asp His Arg Asp Leu Asp Ile Glu Thr His Gly Leu Thr Leu Trp Asp
 420 425 430

Leu Asp Arg Thr Phe His Val Gly Gly Phe Gly Gly Lys Glu Thr Met
 435 440 445

Thr Leu Arg Glu Val Leu Ser Arg Leu Arg Ala Ala Tyr Thr Leu Lys
 450 455 460

Val Gly Ser Glu Tyr Thr His Ile Leu Asp Arg Asp Glu Arg Thr Trp
 465 470 475 480

Leu Gln Asp Arg Leu Glu Ala Gly Met Pro Lys Pro Thr Ala Ala Glu

485	490	495
Gln Lys Tyr Ile Leu Gln Lys Leu Asn Ala Ala Glu Ala Phe Glu Asn		
500	505	510
Phe Leu Gln Thr Lys Tyr Val Gly Gln Lys Arg Phe Ser Leu Glu Gly		
515	520	525
Ala Glu Ser Leu Ile Pro Leu Met Asp Ser Ala Ile Asp Thr Ala Ala		
530	535	540
Gly Gln Gly Leu Asp Glu Val Val Ile Gly Met Pro His Arg Gly Arg		
545	550	555
Leu Asn Val Leu Phe Asn Ile Val Gly Lys Pro Leu Ala Ser Ile Phe		
565	570	575
Asn Glu Phe Glu Gly Gln Met Glu Gln Gly Gln Ile Gly Gly Ser Gly		
580	585	590
Asp Val Lys Tyr His Leu Gly Ser Glu Gly Thr His Leu Gln Met Phe		
595	600	605
Gly Asp Gly Glu Ile Lys Val Ser Leu Thr Ala Asn Pro Ser His Leu		
610	615	620
Glu Ala Val Asn Pro Val Val Glu Gly Ile Val Arg Ala Lys Gln Asp		
625	630	635
Ile Leu Asp Lys Gly Pro Asp Gly Tyr Thr Val Val Pro Leu Leu Leu		
645	650	655
His Gly Asp Ala Ala Phe Ala Gly Leu Gly Ile Val Pro Glu Thr Ile		
660	665	670
Asn Leu Ala Ala Leu Arg Gly Tyr Asp Val Gly Gly Thr Ile His Ile		
675	680	685
Val Val Asn Asn Gln Ile Gly Phe Thr Thr Pro Asp Ser Ser Arg		
690	695	700
S r Met His Tyr Ala Thr Asp Cys Ala Lys Ala Phe Gly Cys Pro Val		
705	710	715
		720

Phe His Val Asn Gly Asp Asp Pro Glu Ala Val Val Trp Val Gly Gln

725

730

735

Leu Ala Thr Glu Tyr Arg Arg Arg Phe Gly Lys Asp Val Phe Ile Asp

740

745

750

Leu Ile Cys Tyr Arg Leu Arg Gly His Asn Glu Ala Asp Asp Pro Ser

755

760

765

Met Thr Gln Pro Lys Met Tyr Glu Leu Ile Thr Gly Arg Asp Ser Val

770

775

780

Arg Ala Thr Tyr Thr Glu Asp Leu Ser Pro Asp Leu Ser Pro

785 790 795 800

Glu Asp Ala Glu Ala Val Val Arg Asp Phe His Asp Gln Met Glu Ser

805

810

815

Val Phe Asn Glu Val Lys Glu Ala Gly Lys Lys Gln Pro Asp Glu Gln

820

825

830

Thr Gly Ile Thr Gly Ser Gln Glu Leu Thr Arg Gly Leu Asp Thr Asn

835

840

845

Ile Thr Arg Glu Glu Leu Val Glu Leu Gly Gln Ala Phe Val Asn Thr

850

855

860

Pro Glu Gly Phe Thr Tyr His Pro Arg Val Ala Pro Val Ala Lys Lys

865 870 875 880

Arg Ala Glu Ser Val Thr Glu Gly Gly Ile Asp Trp Ala Trp Gly Glu

885

890

895

Leu Ile Ala Phe Gly Ser Leu Ala Thr Ser Gly Arg Leu Val Arg Leu

900

905

910

Ala Gly Glu Asp Ser Arg Arg Gly Thr Phe Thr Gln Arg His Ala Val

915

920

925

Ala Ile Asp Pro Asn Thr Ala Glu Glu Phe Asn Pro Leu His Glu Leu

930

935

940

Ala Gln Ala Lys Gly Gly Lys Phe Leu Val Tyr Asn Ser Ala Leu

945 950 955 960
 Thr Glu Tyr Ala Gly Met Gly Phe Glu Tyr Gly Tyr S r Val Gly Asn
 965 970 975
 Pro Asp Ala Val Val Ser Trp Glu Ala Gln Phe Gly Asp Phe Ala Asn
 980 985 990
 Gly Ala Gln Thr Ile Ile Asp Glu Tyr Ile Ser Ser Gly Glu Ala Lys
 995 1000 1005
 Trp Gly Gln Thr Ser Ser Val Ile Leu Leu Leu Pro His Gly Tyr Glu
 1010 1015 1020
 Gly Gln Gly Pro Asp His Ser Ser Ala Arg Ile Glu Arg Phe Leu Gln
 1025 1030 1035 1040
 Leu Cys Ala Glu Gly Ser Met Thr Ile Ala Gln Pro Thr Thr Pro Ala
 1045 1050 1055
 Asn Tyr Phe His Leu Leu Arg Arg His Ala Leu Gly Lys Met Lys Arg
 1060 1065 1070
 Pro Leu Val Val Phe Thr Pro Lys Ser Met Leu Arg Asn Lys Ala Ala
 1075 1080 1085
 Thr Ser Ala Pro Glu Glu Phe Thr Glu Val Thr Arg Phe Lys Ser Val
 1090 1095 1100
 Ile Asp Asp Pro Asn Val Ala Asp Ala Ser Lys Val Lys Lys Ile Met
 1095 1110 1115 1120
 Leu Cys Ser Gly Lys Ile Tyr Tyr Glu Leu Ala Lys Arg Lys Glu Lys
 1125 1130 1135
 Asp Asn Arg Asp Asp Ile Ala Ile Val Arg Ile Glu Met Leu His Pro
 1140 1145 1150
 Ile Pro Phe Asn Arg Leu Arg Asp Ala Phe Asp Gly Tyr Pro Asn Ala
 1155 1160 1165
 Glu Glu Ile Leu Phe Val Gln Asp Glu Pro Ala Asn Gln Gly Ala Trp
 1170 1175 1180

Pro Phe Tyr Gln Glu His Leu Pro Asn Leu Ile Glu Gly Met Leu Pro
 185 1190 1195 1200
 Met Arg Arg Ile Ser Arg Arg Ser Gln Ser Ser Thr Ala Thr Gly Ile
 ... 1205 1210 1215
 Ala Lys Val His Thr Ile Glu Gln Gln Lys Leu Leu Asp Asp Ala Phe
 1220 1225 1230

Asn Ala

【0101】
 <210> 35

(0101)

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for aceA

<400> 35

cctctaccca gcgaactccg 20

【0102】

<210> 36

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for aceA

<400> 36

ctgccttgaa ctcacggttc 20

【0103】

<210> 37

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for accBC

<400> 37

catccacccc ggctacggct

20

【0104】

<210> 38

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for accBC

<400> 38

cggtgactgg gtgttccacc

20

【0105】

<210> 39

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for dtsR1

<400> 39

acggcccccagc cctgaccgac 20

[0106]

<210> 40

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for dtsR1

<400> 40

agcagcgccc atgacggcga 20

[0107]

<210> 41

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for dtsR2

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[0108]

<210> 42

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer for dtsR2

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agcagcgccc atgacggcga

20

[0109]

<210> 43

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pfk

<400> 43

cgtcatccga ggaatcggtcc

20

[0110]

<210> 44

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pfk

<400> 44

cgtggcggcc catgacctcc

21

【0 1 1 1】

<210> 45

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for scrB

<220>

<221> UNSURE

<222> (3)

<223> n=a or g or c or t

<400> 45

ggncghytba aygaycc

17

【0 1 1 2】

<210> 46

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for scrB

<220>

<221> UNSURE

<222> (18)

<223> n=a r g or c or t

<400> 46

ggrcaytccc acatrtanc

20

[0 1 1 3]

<210> 47

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for gluABCD

<400> 47

ccatccggat ccggcaagtc

20

[0 1 1 4]

<210> 48

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for gluABCD

<400> 48

aatccccatct cgtgggtaac

20

[0 1 1 5]

<210> 49

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pdhA

<400> 49

actgtgtccatgggtcttggccc

23

[0116]

<210> 50

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pdhA

<400> 50

cgcgtggaatccgaacatcgaa

20

[0117]

<210> 51

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pc

<400> 51

ggcgcaacct acgacgttgc aatgcg

26

【0118】

<210> 52

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pc

<400> 52

tggccgcctg ggatctcgta

20

【0119】

<210> 53

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for ppc

<400> 53

ggttcctgga ttggtgaga

20

【0120】

<210> 54

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for ppc

<400> 54

ccggccatcct tgttggaatc

20

[0 1 2 1]

<210> 55

<211> 20

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for acn

<220>

<221> UNSURE

<222> (3,6,9)

<223> n=inosine

<400> 55

gtnggnacng aytcsatac

20

[0 1 2 2]

<210> 56

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer for acn

<220>

<221> UNSURE

<222> (3,9,18)

<223> n=inosine

<400> 56

gcnggagana tgtgrtcngt

20

<210> 57

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for icd

<400> 57

gacatttcac tcgctggacg

20

[0 1 2 4]

<210> 58

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for icd

<400> 58

ccgtactctt cagccttctg 20
【0125】
<210> 59
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for lpd

<400> 59
atcatcgcaa ccggttc 17
【012-6】
<210> 60
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for lpd

<400> 60
cgtcaccgat ggcgtaaat 19
【0127】
<210> 61
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for odhA

<400> 61

acaccgtggc cgcctcaacg

20

—[0-1-2-8]—

<210> 62

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for odhA

<400> 62

tgctaacccg tcccacctgg

20

[0 1 2 9]

<210> 63

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
screening PCR of lpd

<400> 63

tacgaggagc agatcctcaa

20

[0 1 3 0]

<210> 64

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
screening PCR of lpd

<400> 64

ttgacgccgg tggctccag

20

[0 1 3 1]

<210> 65

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
LA cloning of acn

<400> 65

ggtaagcta agtagtttc

20

[0 1 3 2]

<210> 66

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
LA cloning of acn

<400> 66

-agctactaaa-cctgcacc-- 18

[0133]

<210> 67

<211> DNA

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
LA cloning of icd

<400> 67

ccgtactttt cagccttctg 67

[0134]

<210> 68

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
LA cloning of icd

<400> 68

tcgtccttgt tccacatc

18

【0135】

<210> 69

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for

LA cloning of lpd

<400> 69

atcatcgcaa ccggttc

17

【0136】

<210> 70

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for

LA cloning of lpd

<400> 70

tacgaggagc agatcctcaa

20

【0137】

<210> 71

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
LA cloning of acn

<400> 71

gctaaactact tagtttcacc

20

[0138]

<210> 72

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
LA cloning of acn

<400> 72

gaaccaggaa ctattgaacc

20

[0139]

<210> 73

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
LA cloning of icd

<400> 73

tccgatgtca tcatcgac

18

[0140]

<210> 74

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
LA cloning of icd

<400> 74

atgtggaaaca aggacgac

18

[0141]

<210> 75

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
LA cloning of odhA

<400> 75

gtacatattg tcgttagaac gcgtaatacg actca

35

[0142]

<210> 76

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

--<223>-Description of Artificial Sequence: primer for
LA cloning of odhA

<400> 70

cgttagaacg cgtaatacga ctcactatag ggaga

35

【書類名】要約書

【要約】

【課題】コリネバクテリウム・サーモアミノゲネス由来のL-アミノ酸合成系酵素、好ましくはコリネバクテリウム・グルタミカムよりも高い温度で機能する酵素をコードする遺伝子を提供する。

【解決手段】一目的とする遺伝子に対応する種々の微生物の既知の遺伝子配列の間でアミノ酸レベルで保存されている領域に基づいて設計した複数組のプライマーとして、コリネバクテリウム・サーモアミノゲネスの染色体DNAを鑄型としてPCRを行い、增幅断片が得られたプライマーをスクリーニング用プライマーに用いて、コリネバクテリウム・サーモアミノゲネスの染色体DNAのプラスミドライブラーから、目的とするDNA断片を含むクローンを選択する。

【選択図】なし

出願人履歴情報

識別番号 [00000066]

1. 変更年月日 1991年 7月 2日

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